

GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 12:44:54 ; Search time 1420 Seconds

(without alignments)  
1129.122 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508  
Sequence: 1 MDVQPKIKHRCFCVSKH.....LNFSGPYQKKPVEKKEVL 99

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODU=frame+ p2n model -DEV=xlp  
-O=/gen2.1/USPTO\_spool/US09801115/tunat\_20062003.141103\_13596/app.query.fasta.1.263  
-DB=EST -QFMT=fastp -SUFFIX=first -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human4.0 -cdi -LIST=45  
-DOCALIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09801115.ecgn.1.1.2874 @tunat.20062003.141103.13596 -MCPU=6 -ICPU=3  
-NO\_MAP -LARGEDEVEX -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

EST :  
1: em\_estba :  
2: em\_esthum :  
3: em\_estlin :  
4: em\_estlun :  
5: em\_estov :  
6: em\_estpl :  
7: em\_estro :  
8: em\_hic :  
9: gb\_est1 :  
10: gb\_est2 :  
11: gb\_hic :  
12: gb\_est3 :  
13: gb\_est4 :  
14: gb\_est5 :  
15: em\_estfun :  
16: em\_estom :  
17: gb\_gss :  
18: em\_gss\_hum :  
19: em\_gss\_inv :  
20: em\_gss\_pln :  
21: em\_gss\_vrt :  
22: em\_gss\_fun :  
23: em\_gss\_mam :  
24: em\_gss\_mus :  
25: em\_gss\_other :  
26: em\_gss\_pro :  
27: em\_gss\_rtd :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	508	100.0	386	9 AA911088	AA911088 OK67E01.s
C 2	508	100.0	391	9 AI989739	AI989739 wu2le10.x
C 3	508	100.0	396	10 AW183193	AW183193 xj67f11.x
C 4	508	100.0	399	9 AA516431	AA516431 ne58a03.s
C 5	508	100.0	402	9 AI989747	AI989747 wu2le109.x
C 6	508	100.0	404	13 BM553678	BM553678 AGENCOURT
C 7	508	100.0	409	9 AI826622	AI826622 w35d10.x
C 8	508	100.0	423	9 AI128804	AI128804 g94d08.s
C 9	508	100.0	427	9 AA455042	AA455042 aa04a07.s
C 10	508	100.0	432	9 AA429945	AA429945 zw67f10.s
C 11	508	100.0	452	9 AI078580	AI078580 cz37h05.x
C 12	508	100.0	453	9 AI743235	AI743235 w90a002.x
C 13	508	100.0	468	12 BF109912	BF109912 717f103.x
C 14	508	100.0	510	12 BF399486	BF399486 UI-R-CA1
C 15	508	100.0	524	12 BG705303	BG705303 602687808
C 16	508	100.0	534	12 BG031757	BG031757 602299819
C 17	505	99.4	487	13 BM472086	BM472086 AGENCOURT
C 18	504	99.2	386	9 AA989129	AA989129 or75h10.s
C 19	504	99.2	781	12 BG528072	BG528072 602579169
C 20	504	99.2	962	12 BG249994	BG249994 60262062
C 21	491	96.7	529	12 BF691818	BF691818 602247787
C 22	484	95.3	443	12 BG613984	BG613984 602641513
C 23	480	94.5	432	10 AV759888	AV759888 AV759888
C 24	476.5	93.8	395	9 AI141284	AI141284 q852h10.s
C 25	475	93.5	353	9 AI265924	AI265924 g86a08.x
C 26	475	93.5	930	12 BF203359	BF203359 601865968
C 27	472	92.9	468	14 W52820	W52820 zc35c06.tl
C 28	471.5	92.8	527	9 AA876539	AA876539 o648h08.s
C 29	471.5	92.8	534	14 BO130559	BO130559 j18a06.x
C 30	471.5	92.8	534	14 BO613826	BO613826 j116a04.x
C 31	471.5	92.8	551	9 AA702011	AA702011 z170d02.s
C 32	471.5	92.8	692	11 AF151058	AF151058 Homo sapi
C 33	471.5	92.8	776	10 AV683453	AV683453 AV683453
C 34	471.5	92.7	409	14 N89912	N89912 zb22g09.sl
C 35	467.5	92.0	789	12 BE737159	BE737159 601305091
C 36	465.5	91.6	542	14 BO129993	BO129993 j182h06.x
C 37	463	91.1	543	12 BG532587	BG532587 602562152
C 38	460.5	90.6	678	13 BI561562	BI561562 603256264
C 39	452	89.0	333	9 AA987264	AA987264 os11a06.s
C 40	445.5	87.7	500	9 AI633679	AI633679 tnl1c04.x
C 41	445.5	87.7	654	12 BF791773	BF791773 602251973
C 42	444	87.4	326	9 AI263261	AI263261 qp62b12.x
C 43	442.5	87.1	606	12 W93646	W93646 zdf9d08.sl
C 44	436	85.8	456	12 BE875161	BE875161 601488641
C 45	435	85.6	319	9 AI349474	AI349474 qp72f07.x

## ALIGNMENTS

RESULT 1  
AA911088/c  
LOCUS AA911088 386 bp mRNA linear EST 09-JUN-1998  
DEFINITION OK67E01.s1 NCI\_CGAP\_G44 Homo sapiens cDNA clone IMAGE:1519032 3',  
ACCESSION AA911088  
VERSION AA911088.1 GI:3050378  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 386)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLNI at:  
www.bio.lnlnl.gov/bbrp/image/image.html  
Insert Length: 381 Std Error: 0.00  
Seq primer: -40m13 fwd. EP from Amersham  
High quality sequence stop: 79.  
Location/Qualifiers

FEATURES  
SOURCE

1.386  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1519032"  
/clone\_1lb="NCI-CCAP.GC4"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT7T3  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bernaldo."

## BASE COUNT

ORIGIN 113 a 87 c 81 g 105 t  
Alignment Scores:  
Pred. No.: 4.09e-59 Length: 386  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-801-115B-2 (1-99) x AA911088 (1-386)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
|||||  
DB 357 ATGATACGTCGACGCCGCAAAATAAACATCGCCCTTCCTCAGTGTGAAGGCCAC 298  
QY 21 ValLysMetLeuArgLeuAspIleIleasnSerLeuValThrThrValPheMetLeuIle 40  
|||||  
DB 297 GTGAAGATGCTGCGCTGGATATATCAACTGCTGTACACAGATTCATCTCATC 238  
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
|||||  
DB 237 GTATCTGTGTGGCAGCTATACCAAGAACCAACATTCAGTGTGGGGGGGTCTT 178  
QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspIleValaLeuIleTyrArgLysLeuLeu 80  
|||||  
DB 177 GCACCTGTGACAGCAGTATGCTGTCTGCGCAGCGGGGCCCTTATTACCGGAACCTCTG 118  
QY 81 PheasnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
|||||  
DB 117 TTCAATCCACGCGGTCTTACCAAGAAAGCCTGTGATGATGAAAAAAGAGTTTGG 61

## RESULT 2

AI989739/c 391 bp mRNA linear EST 27-OCT-1999  
LOCUS wu1e10.x1 Soares.Dieckgraefe.colon\_NHCD Homo sapiens cDNA clone  
DEFINITION IMAGE:2520714.3, mRNA sequence.  
ACCESSION AI989739  
VERSION AI989739.1 GI:5836620  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 391)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

## AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnlnl.gov) for further information.  
Seq primer: -40UP from Gibco.

FEATURES  
SOURCE

1.391  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2520714"  
/clone\_1lb="Soares.Dieckgraefe.colon\_NHCD"  
/tissue\_type="colonic mucosa from 3 patients with Crohn's  
disease"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAGTGGAGAGCGGCCGCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and Eco RI and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization. Tissue samples  
provided by Dr. Brian Dieckgraefe (Washington University,  
discleim.wustl.edu); colonic mucosa represents a range of  
disease; involvement from moderate to severe Crohn's  
disease; samples include both perforating (fistulas) and  
non-perforating samples. Library constructed by Bento  
Soares and M. Fatima Bernaldo."

BASE COUNT 113 a 90 c 81 g 107 t  
ORIGIN

Alignment Scores:  
Pred. No.: 4.16e-59 Length: 391  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-801-115B-2 (1-99) x AI989739 (1-391)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
|||||  
DB 358 ATGATACGTCGACGCCGCAAAATAAACATCGCCCTTCCTCAGTGTGAAGGCCAC 299  
QY 21 ValLysMetLeuArgLeuAspIleIleasnSerLeuValThrThrValPheMetLeuIle 40  
|||||  
DB 298 GTGAAGATGCTGCGCTGGATATATCAACTGCTGTACACAGATTCATCTCATC 239  
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
|||||  
DB 238 GTATCTGTGTGGCAGCTATACCAAGAACCAACATTCAGTGTGGGGGGGTCTT 179  
QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspIleValaLeuIleTyrArgLysLeuLeu 80  
|||||  
DB 178 GCACCTGTGACAGCAGTATGCTGTCTGCGCAGCGGGGCCCTTATTACCGGAACCTCTG 119  
QY 81 PheasnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
|||||  
DB 118 TTCAATCCACGCGGTCTTACCAAGAAAGCCTGTGATGATGAAAAAAGAGTTTGG 62

## RESULT 3

AM183193 396 bp mRNA linear EST 18-NOV-1999  
LOCUS xj67f11.x1 Soares\_NFL\_T\_GBC\_SI Homo sapiens cDNA clone  
DEFINITION

IMAGE:2662317 3', mRNA sequence.  
 ACCESSION AM183193  
 VERSION AM183193.1 GI:6451679  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 396)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgaps-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Seq primer: -40up from Glibco.

FEATURES  
 location/Qualifiers  
 1..396  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2662317"  
 /clone.lib="Soares\_NFL\_T\_GBC\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled. Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NH7, and B-cell NCI-CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 115 a 92 c 80 g 109 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4,24e-59 Length: 396  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-801-115B-2 (1-99) x AM183193 (1-396)

QY 1 MetaspasnValGlnProlysilLeysHisArgProPhecysPheSerVallysglyHis 20  
 DB 359 ATGGATTACGTCAGCCGCAAAATTAACATCGCCCTTGTGCTGATGAGTGAAGGCCAC 300

QY 21 VallysmetLeuArgleuAspIleleasnsrLeuValThrValPheMetLeuile 40  
 DB 299 GTGAAGATGCTGCGCGTGTATATATACATCAGTGTACCAAGATATATCATC 240

QY 41 ValSerValLeuAlaLeuileProgluThrThrThrLeuThrValIglyIglyValPhe 60  
 DB 239 GTATCTGTGTGGCACTGATACCAAGAACCAATTCAGTGTGTGAGGGGTGTTT 180

QY 61 AlaLeuValThrAlaValAlcyscysLeuAlaAspGlyAlaLeuiletyrArgysLeu 80  
 DB 179 GCACCTGTGACAGCAATATGCTGTGCGGAGGGGCCCTTATTTACCGGAAGCTTCTG 120

QY PheasnProSerGlyProtyrGlnlyslsProValHisGluIlyslsGluValleu 99  
 DB 81 TTCATCCCAAGCGGCTCTTACCAAGAAAAGCCTGTGATGAGAAAAGAAAGTTTGG 63

RESULT 4  
 AA516431/c  
 LOCUS AA516431 399 bp mRNA linear EST 13-AUG-1997

DEFINITION ne58a03.s1 NCI-CGAP\_C03 Homo sapiens CDNA clone IMAGE:901516 3', mRNA sequence.  
 ACCESSION AA516431  
 VERSION AA516431.1 GI:2255955  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 399)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgaps-remail.nih.gov  
 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www-bio.llnl.gov/bdrp/image/image.html](http://www-bio.llnl.gov/bdrp/image/image.html)  
 Insert length: 527 Std Error: 0.00  
 Seq primer: -40m13 fwd. RT from Amersham.

FEATURES  
 location/Qualifiers  
 1..399  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:901516"  
 /clone.lib="NCI-CGAP\_C03"  
 /sex="pooled"  
 /tissue\_type="colon"  
 /lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization."

BASE COUNT 115 a 94 c 81 g 109 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4,28e-59 Length: 399  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AA516431 (1-399)

QY 1 MetaspasnValGlnProlysilLeysHisArgProPhecysPheSerVallysglyHis 20  
 DB 357 ATGGATTACGTCAGCCGCAAAATTAACATCGCCCTTGTGCTGATGAGTGAAGGCCAC 298

QY 21 VallysmetLeuArgleuAspIleleasnsrLeuValThrValPheMetLeuile 40  
 DB 297 GTGAAGATGCTGCGCGTGTATATATACATCAGTGTGAACACAGATATCATC 238

QY 41 ValSerValLeuAlaLeuileProgluThrThrThrLeuThrValIglyIglyValPhe 60  
 DB 237 GTATCTGTGTGGCACTGATACCAAGAACCAATTCAGTGTGTGAGGGGTGTTT 178

QY 61 AlaLeuValThrAlaValAlcyscysLeuAlaAspGlyAlaLeuiletyrArgysLeu 80  
 DB 177 GCACCTGTGACAGCAATATGCTGTGCGGAGGGGCCCTTATTTACCGGAAGCTTCTG 118

QY PheasnProSerGlyProtyrGlnlyslsProValHisGluIlyslsGluValleu 99  
 DB 81 TTCATCCCAAGCGGCTCTTACCAAGAAAAGCCTGTGATGAGAAAAGAAAGTTTGG 63

Db 117 TTCATCCAGCGGCTCTACCAAGAAAAGCCTGTGCATGAAAGAAAGAGTTTG 61

RESULT 5  
AI989747/c  
LOCUS AI989747  
DEFINITION WU21F09.x1 Soares-Dieckgraebe.colon\_NHCD Homo sapiens cDNA clone IMAGE:2520713 3', mRNA sequence.

ACCESSION AI989747  
VERSION AI989747.1 GI:5836628  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS 1 (bases 1 to 402)  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: 40UP from Gibco.

FEATURES  
source  
1..402  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2520713"  
/clone\_lib="Soares-Dieckgraebe.colon\_NHCD"  
/tissue\_type="colonic mucosa from 3 patients with Crohn's disease"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCACTCTGAACTGCGAGCGCGCCGCTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraebe (Washington University, dieck@u.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 113 a 90 c 82 g 117 t

ORIGIN

Alignment Scores:  
Pred. No.: 4,33e-59 Length: 402  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 9

US-09-801-115B-2 (1-99) x AI989747 (1-402)

QY 1 MetaspasvAlGInProLySIlleLySHIsArpProPhCySPheSerValLySGLyHIs 20  
DB 368 ATGGATTAACGTGCAGCGCAAAATAAACATCGCCCTTGTGCTCACTGTAAGGCGCAC 309

QY 21 ValLySMetLeuAArgLeuAspLlelleAsnSerLeuValThrThrValPheMetLeuIle 40  
DB 308 GTGAAGATGCTGGCGGTGATATATACATCACTGTATACACAGATTCATGCTATC 249

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAlphe 60  
DB 248 GTATCTGTGTGGCACTGATACCAAGAAACACACATTGACAGTTGTGTGAGGGGTGTTT 189

QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraGlyLeuIleu 80  
DB 188 GCACCTTGACAGACAGATGCTGCTTGTCCGACGCGGCCCTTATTATACCGAAGCTTCTG 129

QY 81 PheAsnProSerGlyProTyrgInLySLeuProValHisGluSylsGluValLeu 99  
DB 128 TTCATCCAGCGGCTCTACCAAGAAAAGCCTGTGCATGAAAGAAAGAGTTTG 72

RESULT 6  
BM553628  
LOCUS BM553628  
DEFINITION BM553628 404 bp mRNA linear EST 20-FEB-2002  
ACCESSION AGENCOURT 6541772 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:5740478  
VERSION BM553628  
KEYWORDS BM553628.1 GI:18792524  
EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS 1 (bases 1 to 404)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ARCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LRAM2755 row: h column: 15  
High quality sequence stop: 403.

FEATURES  
source  
1..404  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5740478"  
/clone\_lib="NIH\_MGC\_88"  
/tissue\_type="duodenal adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."

BASE COUNT 121 a 80 c 87 g 116 t

ORIGIN

Alignment Scores:  
Pred. No.: 4,36e-59 Length: 404  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 13

US-09-801-115B-2 (1-99) x BM553628 (1-404)

QY 1 MetaspasvAlGInProLySIlleLySHIsArpProPhCySPheSerValLySGLyHIs 20  
DB 32 ATGGATTAACGTGCAGCGCAAAATAAACATCGCCCTTGTGCTCACTGTAAGGCGCAC 91

QY 21 ValLySMetLeuAArgLeuAspLlelleAsnSerLeuValThrThrValPheMetLeuIle 40  
DB 92 GTGAAGATGCTGGCGGTGATATATATCACTGTAAGCAACAGTATCATGCTATC 151

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAlphe 60  
DB 152 GTATCTGTGTGGCACTGATACCAAGAAACACACATTGACAGTTGTGTGAGGGGTGTTT 211



QY 61 AlaleuValThralaValcysCysLeuAlaaspGlyAlaLeuIleTyArGlySLeu 80  
 Db 212 GCATTGTGACAGAGATGCTGCTTGCAGGGGCGCTTTATTCAGGAAGCTTCTG 271  
 QY 81 PheasnProSerGlyProTyrgLnyLysProValHsGluLysGluValLeu 99  
 Db 272 TTCATCCAGCGGCTCTTACAGAAAAACCTGTGATGAAAAAAGAAAGTTTG 328

RESULT 7  
 A1826623/c 409 bp mRNA linear EST 21-DEC-1999  
 LOCUS w35d10.x1 NCI\_CGAP\_Pt22 Homo sapiens CDNA clone IMAGE:2417395 3'  
 DEFINITION mRNA sequence.  
 ACCESSION A1826623  
 VERSION A1826623.1 GI:5447294  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 409)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnlni.gov/bhrp/image/image.html  
 Insert Length: 462 Std Error: 0.00  
 Seq primer: -400p from Gdbco.  
 Location/Qualifiers  
 1. 409  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:2417395"  
 /clone\_lib="NCI\_CGAP\_Pt22"  
 /sex="male"  
 /tissue\_type="normal prostate"  
 /lab\_host="DH10B"  
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)  
 with a modified polylinker; 1st strand CDNA was prepared  
 from normal prostate bulk tissue, and was then primed with  
 a Not I - oligo(dT) primer. Double-stranded CDNA was  
 ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the  
 modified pT73 vector. Library is normalized, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 112 a 94 c 80 g 123 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4.44e-59 Length: 409  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1826623 (1-409)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPhcCysPheSerValLysGlyHis 20  
 Db 367 ATGGATTAACGTCGACGCGAAATAAATCATGCCCCCTTCCTCAGTGGAAGGCGCAC 308  
 QY 21 VallysMetLeuArgLeuAspIlelleasnsSerLeuValThrValPheMetLeuIle 40

Db 307 GTGAGATGCTCGCGGCTGATATTAACATCACTGATGTAACAGATATTCATCTCATC 248  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAlaPhe 60  
 Db 247 GTATCTGTGTGGACATGATACAGAAACACACACATGACAGTTGGTGGAGGGGTGTTT 188  
 QY 61 AlaleuValThralaValcysCysLeuAlaaspGlyAlaLeuIleTyArGlySLeu 80  
 Db 187 GCATTGTGACAGAGATGCTGCTTGCAGGGGCGCTTTATTCAGGAAGCTTCTG 128

RESULT 8  
 A1128804/c 423 bp mRNA linear EST 05-OCT-1998  
 LOCUS q94d08.s1 Soares\_fetal\_heart\_NbH19w Homo sapiens CDNA clone  
 DEFINITION IMAGE:1694391 3', mRNA sequence.  
 ACCESSION A1128804  
 VERSION A1128804.1 GI:3597318  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 423)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnlni.gov) for further information.  
 Insert Length: 382 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 413.  
 Location/Qualifiers  
 1. 423  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:1694391"  
 /clone\_lib="Soares\_fetal\_heart\_NbH19w"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st  
 strand CDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCATTCGATCGAGTGGAGCGCGCATCTTTTATTTTATTTT 3']  
 TGTACCATTCGATCGAGTGGAGCGCGCATCTTTTATTTTATTTT 3']  
 double-stranded CDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M. Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbH19w."

BASE COUNT 116 a 101 c 89 g 117 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4.66e-59 Length: 423  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1128804 (1-423)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPhcCysPheSerValLysGlyHis 20

Db 353 ATGGATACGTCGACGCCGAAATAAACATCGCCCTTCCTGCTGATGATGAAGCCAC 294  
 QY 21 VallyMetleuAargleuAspIlelleAsnSerleuValThThrValPheMetleu 40  
 Db 293 GTCAAGATCTCGCGCTGATATATCAACTCAGTGTAAACAGTATATTCATGCTCATC 234  
 QY 41 ValSerValleuAlaIleuIleProGluThrThrThrThrThrValGlyGlyValPhe 60  
 Db 233 GATCTGTGTGGCAGTATACAGAAACACACATTCAGCTTGCGAGGCTGTT 174  
 QY 61 AlaIleuValThrAlaValIcysCysLeuAlaAspGlyAlaIleuIleTyArgIysLeu 80  
 Db 173 GCACCTGTGACAGCAGTATGCTGTCTTCCGACGGGCGCTTATTTACCGGAAGCTCTG 114  
 QY 81 PheAsnProSerGlyProTyArgIleIysIysProValHisGluIysGlyValIle 99  
 Db 113 TTCATCCACGCGCTCTTACCAAGAAAGCTGTGATGAAAAAGAGATTG 57

RESULT 9 427 bp mRNA linear EST 06-JUN-1997  
 AA455042/c  
 LOCUS aa04a07.s1 Soares\_NHMPu\_S1 Homo sapiens cDNA clone IMAGE:812244  
 DEFINITION 3' mRNA sequence.  
 ACCESSION AA455042  
 VERSION AA455042.1 GI:2177818  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 427)  
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.  
 TITLE WashU-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -41m13 fwd. ET from Amersham  
 High quality sequence stop: 395.

## FEATURES

## SOURCE

1.427  
 /organism="Homo sapiens"  
 /db\_xref="GDB:6043155"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:812244"  
 /clone.lib="Soares\_NHMPu\_S1"  
 /tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
 /lab\_host="DH10B"  
 /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBH, pregnant uterus 2NBH, and fetal heart 2NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

## BASE COUNT

119 a 101 c 91 g 116 t

## Alignment Scores:

Pred. No.: 4,72e-59 Length: 427  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AA455042 (1-427)

QY 1 MetAspValAlaGlnProIysIleIysHisArgProPheCysPheSerValIysGlyHis 20  
 Db 356 ATGGATACGTCGACGCCGAAATAAACATCGCCCTTCCTGCTGATGATGAAGCCAC 297  
 QY 21 VallyMetleuAargleuAspIlelleAsnSerleuValThThrValPheMetleu 40  
 Db 296 GTCAAGATCTCGCGCTGATATATCAACTCAGTGTAAACAGTATATTCATGCTCATC 237  
 QY 41 ValSerValleuAlaIleuIleProGluThrThrThrThrThrValGlyGlyValPhe 60  
 Db 233 GATCTGTGTGGCAGTATACAGAAACACACATTCAGCTTGCGAGGCTGTT 174  
 QY 61 AlaIleuValThrAlaValIcysCysLeuAlaAspGlyAlaIleuIleTyArgIysLeu 80  
 Db 176 GCACCTGTGACAGCAGTATGCTGTCTTCCGACGGGCGCTTATTTACCGGAAGCTCTG 114  
 QY 81 PheAsnProSerGlyProTyArgIleIysIysProValHisGluIysGlyValIle 99  
 Db 116 TTCATCCACGCGCTCTTACCAAGAAAGCTGTGATGAAAAAGAGATTG 57

RESULT 10 432 bp mRNA linear EST 16-OCT-1997  
 AA429945/c  
 LOCUS zw67f10.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:781291  
 DEFINITION 3' mRNA sequence.  
 ACCESSION AA429945  
 VERSION AA429945.1 GI:2113244  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 432)  
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.  
 TITLE WashU-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -41m13 fwd. ET from Amersham  
 High quality sequence stop: 421.

## FEATURES

## SOURCE

1.432  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:781291"  
 /clone.lib="Soares\_testis\_NHT"  
 /sex="male"  
 /lab\_host="DH10B"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGACAGTGGAGCGGCGCCCAATTTTATTTTATTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot's, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 119 a 101 c 92 g 120 t

ORIGIN

# Alignment Scores:

Pred. No.:	Length:	432
Score:	508.00	Matches: 99
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0

US-09-801-115b-2 (1-99) x AA429945 (1-432)

QY 1 MetaspasnaValGlnProlystIleYshIstArgProPhcysPheSerValIysGlyHis 20  
 DB 361 ATGATTAACGTGCGCGGAAATTAACATCGCCCTTCCTTCAGTGTGAAGGCCAC 302  
 QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerIleValThrThrValPheMetLeu 40  
 DB 301 GTGAGATGCTGCGCGGATATATCACTGCTGTAACAACAGATTTCATGCTCATC 242  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 DB 241 GTACTGTGTGGACGATACGATACGAAACCAACATGACAGTGTGAGGGGTCTT 182  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgIysLeu 80  
 DB 181 GCACCTGTGACAGAGATGCTGCTGCCGACGCGGCCCTTATTACCGGAACCTCTG 122  
 QY 81 PheAsnProSerGlyProTyrGlnIlystIysProValHisGluIysGluValLeu 99  
 DB 121 TTCATCCACGGCTCTTACCAAGAAAGCCGTGTGATGAAGAAAGATTGTG 65

RESULT 11  
 A1078580/c

LOCUS 452 bp mRNA linear EST 10-AUG-1998  
 DEFINITION 0237h05.x1 Soares\_NbHMPu\_S1 Homo sapiens cDNA clone IMAGE:1677561  
 3', mRNA sequence.

ACCESSION A1078580  
 VERSION A1078580.1 GI:3412988  
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 452)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

NOTE: This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 410.

Location/Qualifiers

FEATURES

SOURCE

1. .452  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1677561"  
 /clone\_lib="Soares\_NbHMPu\_S1"  
 /tissue\_type="Pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /note="Organ: mixed (see below); Vector: pT73D-Pac  
 (Pharmacia) with a modified polylinker; Site\_1: Not I;  
 Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NBH, pregnant uterus  
 NbHPU, and fetal heart NbH19W) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 26032-265223, 340488-345479, and 484488-489479. "

BASE COUNT 125 a 110 c 97 g 120 t

ORIGIN

# Alignment Scores:

Pred. No.:	Length:	452
Score:	5126-59	Matches: 99
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0

US-09-801-115b-2 (1-99) x A1078580 (1-452)

QY 1 MetaspasnaValGlnProlystIleYshIstArgProPhcysPheSerValIysGlyHis 20  
 DB 359 ATGATTAACGTGCGCGGAAATTAACATCGCCCTTCCTTCAGTGTGAAGGCCAC 300  
 QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerIleValThrThrValPheMetLeu 40  
 DB 299 GTGAGATGCTGCGCGGATATATCACTGCTGTAACAACAGATTTCATGCTCATC 240  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 DB 239 GTATCTGTGTGGACGATACGATACGAAACCAACATGACAGTGTGAGGGGTCTT 180  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgIysLeu 80  
 DB 179 GCACCTGTGACAGAGATGCTGCTGCCGACGCGGCCCTTATTACCGGAACCTCTG 120  
 QY 81 PheAsnProSerGlyProTyrGlnIlystIysProValHisGluIysGluValLeu 99  
 DB 119 TTCATCCACGGCTCTTACCAAGAAAGCCGTGTGATGAAGAAAGATTGTG 63

RESULT 12  
 A1743235/c

LOCUS 453 bp mRNA linear EST 20-DEC-1999  
 DEFINITION W990802.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
 IMAGE:2372330 3', mRNA sequence.

ACCESSION A1743235  
 VERSION A1743235.1 GI:5111523  
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 453)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

NOTE: This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.

Insert Length: 378 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

FEATURES

SOURCE

1. .453  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2372330"  
 /clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized  
 libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 123 a 109 c 93 g 128 t  
ORIGIN

## Alignment Scores:

Pred. No.: 5.14e-59 Length: 453  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-801-115b-2 (1-99) x AT743235 (1-453)

QY 1 MetaspasnValGlnProLysIleLysHISArgProPhcysPheSerValLysGlyHis 20  
|||||  
362 ATGATTAACGTCGACGCCGAAATTAACAATCGCCCTTCGCTTCACTGTAAGAGCCAC 303

QY 21 ValLysMetLeuArgLeuAspIleLeuSerLeuValThrThyValPheMetLeuIle 40  
|||||  
302 GTGAAGATCGTCGGCGGTGATATTAACAACCTGATCAACAGTATTCATGCTCATC 243

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
|||||  
242 GTATCTGTGTGGCACTGATACCAACCAACCACTTACAGCTTGCGAGGGGTGTT 183

QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeu 80  
|||||  
182 GCACCTGTGACAGCACTATGCTGTCCGACGGGGCCCTTATTACCGAAGCTTCG 123

QY 81 PheAsnProSerGlyProTyArgLysLysProValHisGluLysLysGluValLeu 99  
|||||  
122 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAGAAAGAGTTTG 66

RESULT 13 468 bp mRNA linear EST 20-OCT-2000  
BF109912/c  
LOCUS  
DEFINITION  
7171f03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
IMAGE:3526805 3' similar to TR:Q90I41 Q90I41 CHEMOKINE-LIKE FACTOR  
1. (1) ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
BF109912  
BF109912.1 GI:10939602  
EST.

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40up from Gibco.

FEATURES  
source  
1..468  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3526805"

/clone\_11b="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
/lab\_host="DH10B"  
/note="Organ: pooled; Vector: pUT73D-Pac (pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Equal amounts of plasmid DNA from five normalized  
libraries were mixed, and ss circles were made in vitro.  
Following HAP purification, this DNA was used as tracer in  
a subtractive hybridization reaction. The driver was  
PCR-amplified cDNAs from pools of 5,000 clones made from  
the same 5 libraries. The pools consisted of the following  
libraries and clones: Soares NBHSF pool 1:  
309384-310919, 323208-325895 Soares NB2HP pool 1:  
145032-147335, 147720-148103, 148872-149255, 15002 -  
150407, 151176-152327 Soares NB2HF8-9W pool 1:  
758280-760583, 772104-774407 Soares NBHPA pool 1:  
304776-306311, 320136-322823, 326280-326663 Soares NBHOT  
pool 1: 723720-726407, 739080-740999 Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 127 a 116 c 102 g 123 t  
ORIGIN

## Alignment Scores:

Pred. No.: 5.39e-59 Length: 468  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-801-115b-2 (1-99) x BF109912 (1-468)

QY 1 MetaspasnValGlnProLysIleLysHISArgProPhcysPheSerValLysGlyHis 20  
|||||  
362 ATGATTAACGTCGACGCCGAAATTAACAATCGCCCTTCGCTTCACTGTAAGAGCCAC 303

QY 21 ValLysMetLeuArgLeuAspIleLeuSerLeuValThrThyValPheMetLeuIle 40  
|||||  
302 GTGAAGATCGTCGGCGGTGATATTAACAACCTGATCAACAGTATTCATGCTCATC 243

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
|||||  
242 GTATCTGTGTGGCACTGATACCAACCAACCACTTACAGCTTGCGAGGGGTGTT 183

QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeu 80  
|||||  
182 GCACCTGTGACAGCACTATGCTGTCCGACGGGGCCCTTATTACCGAAGCTTCG 123

QY 81 PheAsnProSerGlyProTyArgLysLysProValHisGluLysLysGluValLeu 99  
|||||  
122 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAGAAAGAGTTTG 66

RESULT 14 510 bp mRNA linear EST 27-NOV-2000  
BF399486/c  
LOCUS  
DEFINITION  
UI-R-CA1-bjb-b-12-0-UI-s1 UI-R-CA1 Rattus norvegicus cDNA clone  
IMAGE:3526805 3' similar to TR:Q90I41 Q90I41 CHEMOKINE-LIKE FACTOR  
1. (1) ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
BF399486  
BF399486.1 GI:11384494  
EST.

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae;  
Rattus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 510)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

FEATURES  
source  
1..468  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3526805"

451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: mscores@blue.wesg.uiowa.edu

The sequence contained an oligo-dt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares lab clone distribution: clones will be available through Research Genetics (www.resgen.com)  
Seq primer: M13 Forward  
POLA-les.

## FEATURES

source

Location/Qualifiers  
1. 510  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-CAL-b-12-0-UI"  
/lab\_host="UI-R-CAL"  
/note="Vector: pMT3D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-CAL library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at [ratest.eng.uiowa.edu](http://ratest.eng.uiowa.edu). The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)  
TAG\_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t  
ORIGIN

## Alignment Scores:

Pred. No.: 6,09e-59 Length: 510  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-801-115B-2 (1-99) x BF399486 (1-510)

QY 1 Metaspasnavalglnprolysilleyshisargprophycyspheservallysglyhis 20  
|||||  
DB 371 ATGGATACGTGCGAGCCGAAATAAATCAATCGCCCTCTGCTTCAGTGAAGGCCAC 312  
|||||  
QY 21 VallysMetleuargleuaspllelleasnserleuvalthrthrvalphemetleuile 40  
|||||  
DB 311 GTGAAGATGTCGGCGTGATATTATCAACTGCTGTAACACAGATATTCATCTCATC 252  
|||||  
QY 41 ValserValleualaleuileprogluthrthrthrleuthrvaliglyglyvalphe 60  
|||||  
DB 251 GTACTGTGTGGCAGCTATACAGAAACCAACATTCAGTGGTGGGGGTGT 192  
|||||  
QY 61 Alaleuvalthrvalalacyscysleualaspolyalaleuiletyrarglyleu 80  
|||||  
DB 191 GCACCTGTGACAGCAGATGCTGCTGCTGCGACGGGGCCCTTATTACCGGAAGCTCTG 132  
|||||  
QY 81 PheasnProserglyprotyrglnlylsysprovalhisgilylsysgluvalleu 99  
|||||  
DB 131 TTCAATCCACGCGTCTTACCAAGAAAAGCCTGTGATGAAAAAAGAGTTT 75  
|||||

## RESULT 15

LOCUS 524 bp mRNA linear EST 07-MAY-2001  
DEFINITION 602687808P1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:4820568 5',  
mRNA sequence.

ACCESSION BG705303  
VERSION BG705303.1 GI:13979504  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC  
TITLE NIH-MGC  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabes-remail.nih.gov

Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LAM10725 row: 0 column: 01  
High quality sequence stop: 521.

## FEATURES

source

Location/Qualifiers  
1. 524  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4820568"  
/clone\_id="NIH\_MGC\_95"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcag)  
); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTT-3',  
size-selected for average insert size 2.5 kb and  
normalized to R0F 5. This is a primary library enriched  
for full-length clones and constructed using the  
Cap-trapper method (Carninci, in preparation). Library  
constructed by M. Brownstein (NIH/NHGRI, National  
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 142 a 133 c 138 g 131 t  
ORIGIN

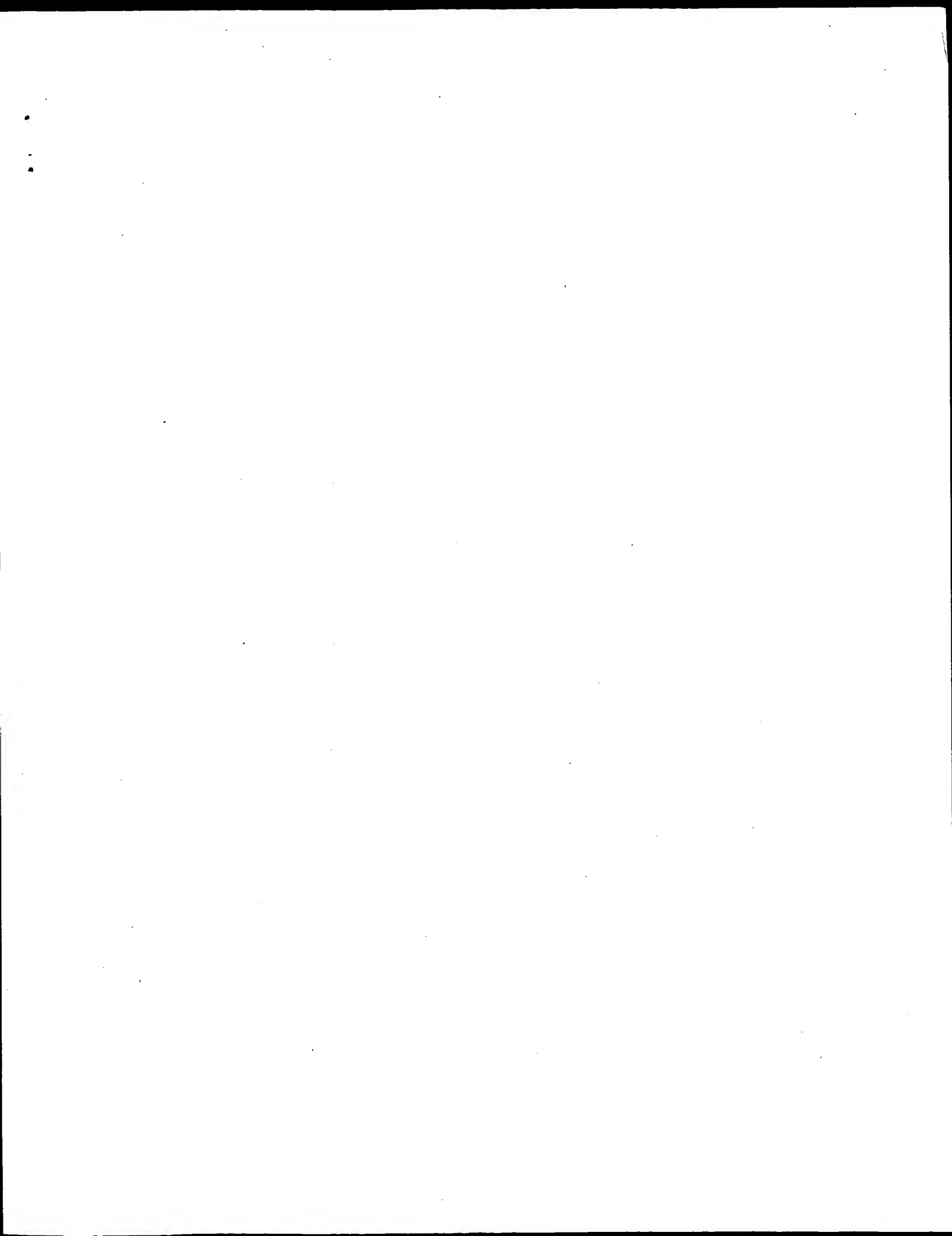
## Alignment Scores:

Pred. No.: 6,33e-59 Length: 524  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-801-115B-2 (1-99) x BG705303 (1-524)

QY 1 Metaspasnavalglnprolysilleyshisargprophycyspheservallysglyhis 20  
|||||  
DB 141 ATGGATACGTGCGAGCCGAAATAAATCAATCGCCCTCTGCTTCAGTGAAGGCCAC 200  
|||||  
QY 21 VallysMetleuargleuaspllelleasnserleuvalthrthrvalphemetleuile 40  
|||||  
DB 201 GTGAAGATGTCGGCGTGATATTATCAACTGCTGTAACACAGATATTCATGCTCATC 260  
|||||  
QY 41 ValserValleualaleuileprogluthrthrthrleuthrvaliglyglyvalphe 60  
|||||  
DB 261 GTACTGTGTGGCAGCTATACAGAAACCAACATTCAGTGGTGGGGGTGT 320  
|||||  
QY 61 Alaleuvalthrvalalacyscysleualaspolyalaleuiletyrarglyleu 80  
|||||  
DB 321 GCACCTGTGACAGCAGATGCTGCTGCTGCGACGGGGCCCTTATTACCGGAAGCTCTG 380  
|||||  
QY 81 PheasnProserglyprotyrglnlylsysprovalhisgilylsysgluvalleu 99  
|||||  
DB 381 TTCAATCCACGCGTCTTACCAAGAAAAGCCTGTGATGAAAAAAGAGTTT 437  
|||||

Search completed: June 25, 2003, 13:38:30  
Job time: 1425 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 11:54:40 ; Search time 215 Seconds

(without alignments)  
1036.967 Million cell updates/sec

Title:

US-09-801-115B-2

Perfect score:

508

Sequence: 1 MDWQPKIRKHPFCFSVKGH.....LFPSPGYOKPKVHEKKEVL 99

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODPL-frame+ p2n model -DEV-xlp  
-Q/cgn2.1/USPFO.spool/us0901115/runat\_20062003\_141102\_13575/app\_query.fasta.1.263  
-DB-NGeneseq\_101002 -QFWT-fastap -SUFFIX-rng -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdl  
-LIST=45 -DOCALLIGN=200 -THR.SCORE-Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15  
-MOD-LOCAL -OUTPMT-PRO -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US0901115.ecgn.1.1.396 -runat 20062003\_141102\_13575 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGESOURCY -NEG\_SCORES=0 -NMT -DSPBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq\_101002:\*  
1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
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22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	508	100.0	413	20	AAK97873	Human secreted pro
2	508	100.0	439	24	ABK36006	Human sequence #397
3	508	100.0	504	19	AAV59598	Human secreted pro
4	508	100.0	506	19	AAV59746	Human secreted pro
5	508	100.0	515	21	AAK87730	Human secreted pro
6	508	100.0	515	22	AAK64012	Human secreted pro
7	508	100.0	534	21	AAK38006	Human secreted pro
8	508	100.0	538	22	AAK98515	Human secreted pro
9	508	100.0	538	22	AAK98548	Human secreted pro
10	508	100.0	558	22	AAK34835	Human secreted pro
11	508	100.0	555	22	AAK44932	Human secreted pro
12	504	99.2	297	21	AAK15919	Human secreted pro
13	504	99.2	467	21	AAK15929	Human secreted pro
14	489	96.3	500	20	AAK97826	Human secreted pro
15	471.5	92.8	459	21	AAK38007	Human secreted pro
16	471.5	92.8	637	21	AAK56747	Human secreted pro
17	471.5	92.8	663	20	AAK34051	Human secreted pro
18	471.5	92.8	663	21	AAK78498	Human secreted pro
19	471.5	92.8	663	21	AAK58238	Human secreted pro
20	471.5	92.8	669	21	AAK87771	Human secreted pro
21	471.5	92.8	669	22	AAK64053	Human secreted pro
22	471.5	92.8	670	24	AB190366	Human secreted pro
23	471.5	92.8	908	22	AAK44933	Human secreted pro
24	467.5	92.0	638	24	ABK35884	Human secreted pro
25	461	90.7	415	21	AAK00147	Human secreted pro
26	357	70.3	392	21	AAK16090	Human secreted pro
27	339.5	66.8	363	21	AAK38009	Human secreted pro
28	339.5	66.8	566	22	AAK45120	Human secreted pro
29	339.5	66.8	566	22	AAK45121	Human secreted pro
30	331	65.2	204	21	AAK38008	Human secreted pro
31	323	63.1	311	20	AAK97851	Human secreted pro
32	318.5	62.7	495	20	AAK34052	Human secreted pro
33	318.5	62.7	495	21	AAK78499	Human secreted pro
34	318.5	62.7	495	22	AAK93358	Human secreted pro
35	317	62.4	334	20	AAK41509	Human secreted pro
36	294	57.9	379	21	AAK41312	Human secreted pro
37	257.5	50.7	465	22	ABK09082	Human secreted pro
38	245	48.2	207	24	ABK94246	Human secreted pro
39	245	48.2	207	24	ABK62782	Human secreted pro
40	245	48.2	207	24	ABK62959	Human secreted pro
41	245	48.2	207	24	ABK63180	Human secreted pro
42	215	42.3	2953	22	AAK68359	Human secreted pro
43	215	42.3	2953	22	AAK68360	Human secreted pro
44	211	41.5	13744	22	AAK68361	Human secreted pro
45	211	41.5	13744	22	AAK82406	Human secreted pro

## ALIGNMENTS

RESULT 1  
AAK97873 standard; CDNA: 413 BP.

AAK97873;  
23-SEP-1999 (first entry)

Human secreted protein encoding CDNA #61.

Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;  
diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

Homo sapiens.

WO9925825-A2.

27-MAY-1999.



XX PF 13-NOV-1998; 98MO-IB01862.  
 XX PR 04-SEP-1998; 98US-0099273.  
 XX PR 13-NOV-1997; 97US-0066677.  
 XX PR 17-DEC-1997; 97US-0069957.  
 XX PR 09-FEB-1998; 98US-0074121.  
 XX PR 13-APR-1998; 98US-0081563.  
 XX PR 10-AUG-1998; 98US-0096116.  
 XX PA (GEST ) GENSET.  
 XX PI Bouquelert L, DucJert A, Dumas Mline Edwards J;  
 XX DR WPI: 1999-347472/29.  
 XX DR P-PSDB; AAY36189.  
 XX PS Extended CDNA's encoding secreted proteins  
 XX PS Claim 1; Page 261; 307pp; English.  
 XX CC AAY97813-X97906 represent extended CDNA's which encode novel human  
 CC secreted proteins (see AAY36129-Y36222) and which have cytosolic,  
 CC thrombotic and osteopathic activity. The extended CDNA's can be used to  
 CC express secreted proteins or parts of them or to obtain antibodies  
 CC capable of binding to the secreted proteins. They may also be used in  
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC Uses also include design of expression vectors and secretion vectors.  
 XX CC  
 SQ Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.04e-58 Length: 413  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0  
 US-09-801-115B-2 (1-99) x AAY97873 (1-413)  
 QY 1 MetaspasValGlnProlysllelyshsArpProphcysPheSerVallyglyHis 20  
 DB 46 ATGATTAACGTCGACGCCGAAATTAACATCGCCCTTCTGCTCAAGTGAAGGCCAC 105  
 QY 21 VallysmetLeuArgleuAspIleleasnSerleuValThrThrValPheMetLeuIle 40  
 DB 106 GTGAAGATGCTGCGGCTGATATATCACTCACTGTAACAACAGATTCATCTCATC 165  
 QY 41 ValSerValleuAlaIleuIleProGluThrThrThrleuThrValGlyGlyValPhe 60  
 DB 166 GTATCTGTGTGGACAGTATACAGAAACCAACCAATGACAGTTGGTGAAGGGGTGTTT 225  
 QY 61 AlaleuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeu 80  
 DB 226 GCACTGTGACAGAGATGCTGCTGCCGACGAGGGGCCCTTATTTACCCGAAGCTTCTG 285  
 QY 81 PheasnProSerGlyProTyrgLlnLysLysProValHisGluLysGluValLeu 99  
 DB 286 TTCAATCCCAAGCGGTCTTACACAGAAAGCCGTGATGATAAAAAAGAAAGTTTTC 342  
 RESULT 2  
 ABR36006  
 ID ABR36006 standard; CDNA: 439 BP.  
 AC ABR36006;  
 XX 08-MAY-2002 (first entry)  
 DT CDNA sequence #397 encoding novel human secreted protein.  
 DE Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
 XX Immune deficiency disorder; blood disorder; inflammatory disorder;  
 KW

KW KW infectious disorder; allergic condition; neurodegenerative disorder;  
 KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;  
 KW tumour; cancer; hepatotropic; immunosuppressive; antineumatic; gene; ss.  
 XX OS Homo sapiens.  
 XX MO200177289-A2.  
 XX PN 18-OCT-2001.  
 XX PD 29-MAR-2001; 2001MO-US10232.  
 XX PF 06-APR-2000; 2000US-195605P.  
 XX PR (GEMV ) GENETICS INST INC.  
 XX PA Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MT, Bowman MR, Spaulding V, Wong GG;  
 PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;  
 XX DR WPI: 2002-179322/23.  
 XX PT Six hundred and twenty three polynucleotides derived from a variety of  
 PT human tissue sources which encode secreted proteins, useful for  
 PT treating immune deficiencies and disorders such as autoimmune disorders  
 PS Claim 1; Page 296-297; 393pp; English.  
 XX CC The present invention relates to the isolation of novel CDNA sequences  
 CC which encode human secreted proteins. The CDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopenia), inflammatory  
 CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),  
 CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.  
 CC haemophilia), and tumours. The polynucleotide sequences of the  
 CC invention are also useful in gene therapy. ABR3610-ABR36232 represent  
 CC the CDNA sequences of the invention that encode for novel human  
 CC secreted proteins.  
 XX CC  
 SQ Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.64e-58 Length: 439  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-801-115B-2 (1-99) x ABR36006 (1-439)  
 QY 1 MetaspasValGlnProlysllelyshsArpProphcysPheSerVallyglyHis 20  
 DB 81 ATGATTAACGTCGACGCCGAAATTAACATCGCCCTTCTGCTCAAGTGAAGGCCAC 140  
 QY 21 VallysmetLeuArgleuAspIleleasnSerleuValThrThrValPheMetLeuIle 40  
 DB 141 GTGAAGATGCTGCGGCTGATATATCACTCACTGTAACAACAGTTCATCTCATC 200  
 QY 41 ValSerValleuAlaIleuIleProGluThrThrThrleuThrValGlyGlyValPhe 60  
 DB 201 GTATCTGTGTGGACAGTATACAGAAACCAACCAATGACAGTTGGTGAAGGGGTGTTT 260  
 QY 61 AlaleuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeu 80  
 DB 261 GTATCTGTGTGGACAGTATACAGAAACCAACCAATGACAGTTGGTGAAGGGGTGTTT 320

DB 261 GCACCTGTGACAGCAGTATGCTGTGCGACGAGGCGCCCTTATTACCGAGCTTCTG 320  
QY 81 PheanProSerGlyProTyrGlnLysPyrroValHisGlnLysLysGlnValLeu 99  
DB 321 TTCAATCCACGAGGCTCTTACACGAAAAAGCGCTGTGATGAAAAAAGAGTTTGG 377  
RESULT 3  
AAV59598 standard: DNA; 504 BP.  
XX AAV59598;  
AC AAV59598;  
XX  
DI 06-JAN-1999 (first entry)  
XX  
DE Human secreted protein gene 88 clone HAUAV32.  
XX  
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX  
XX Homo sapiens.  
OS  
PN WO9839448-A2.  
XX  
PD 11-SEP-1998.  
XX  
PF 06-MAR-1998; 98WO-US04493.  
XX  
XX 02-OCT-1997; 97US-0061060.  
PR 07-MAR-1997; 97US-0038621.  
PR 07-MAR-1997; 97US-0040161.  
PR 07-MAR-1997; 97US-0040162.  
PR 07-MAR-1997; 97US-0040163.  
PR 07-MAR-1997; 97US-0040333.  
PR 07-MAR-1997; 97US-0040334.  
PR 07-MAR-1997; 97US-0040336.  
PR 07-MAR-1997; 97US-0040626.  
PR 11-APR-1997; 97US-0043311.  
PR 11-APR-1997; 97US-0043312.  
PR 11-APR-1997; 97US-0043313.  
PR 11-APR-1997; 97US-0043314.  
PR 11-APR-1997; 97US-0043356.  
PR 11-APR-1997; 97US-0043569.  
PR 11-APR-1997; 97US-0043576.  
PR 11-APR-1997; 97US-0043578.  
PR 11-APR-1997; 97US-0043580.  
PR 11-APR-1997; 97US-0043670.  
PR 11-APR-1997; 97US-0043671.  
PR 11-APR-1997; 97US-0043672.  
PR 11-APR-1997; 97US-0043674.  
PR 23-MAY-1997; 97US-0047592.  
PR 23-MAY-1997; 97US-0047500.  
PR 23-MAY-1997; 97US-0047501.  
PR 23-MAY-1997; 97US-0047502.  
PR 23-MAY-1997; 97US-0047503.  
PR 23-MAY-1997; 97US-0047581.  
PR 23-MAY-1997; 97US-0047582.  
PR 23-MAY-1997; 97US-0047583.  
PR 23-MAY-1997; 97US-0047584.  
PR 23-MAY-1997; 97US-0047585.  
PR 23-MAY-1997; 97US-0047586.  
PR 23-MAY-1997; 97US-0047587.  
PR 23-MAY-1997; 97US-0047588.  
PR 23-MAY-1997; 97US-0047589.  
PR 23-MAY-1997; 97US-0047590.  
PR 23-MAY-1997; 97US-0047592.  
PR 23-MAY-1997; 97US-0047593.

PR 23-MAY-1997; 97US-0047594.  
PR 23-MAY-1997; 97US-0047595.  
PR 23-MAY-1997; 97US-0047596.  
PR 23-MAY-1997; 97US-0047597.  
PR 23-MAY-1997; 97US-0047598.  
PR 23-MAY-1997; 97US-0047599.  
PR 23-MAY-1997; 97US-0047600.  
PR 23-MAY-1997; 97US-0047601.  
PR 23-MAY-1997; 97US-0047612.  
PR 23-MAY-1997; 97US-0047613.  
PR 23-MAY-1997; 97US-0047614.  
PR 23-MAY-1997; 97US-0047615.  
PR 23-MAY-1997; 97US-0047617.  
PR 23-MAY-1997; 97US-0047618.  
PR 23-MAY-1997; 97US-0047632.  
PR 23-MAY-1997; 97US-0047633.  
PR 06-JUN-1997; 97US-0048964.  
PR 06-JUN-1997; 97US-0048974.  
PR 13-JUN-1997; 97US-0049610.  
PR 08-JUL-1997; 97US-0051926.  
PR 16-JUL-1997; 97US-0052874.  
PR 18-AUG-1997; 97US-0055724.  
PR 22-AUG-1997; 97US-0056630.  
PR 22-AUG-1997; 97US-0056631.  
PR 22-AUG-1997; 97US-0056632.  
PR 22-AUG-1997; 97US-0056636.  
PR 22-AUG-1997; 97US-0056637.  
PR 22-AUG-1997; 97US-0056662.  
PR 22-AUG-1997; 97US-0056664.  
PR 22-AUG-1997; 97US-0056845.  
PR 22-AUG-1997; 97US-0056846.  
PR 22-AUG-1997; 97US-0056862.  
PR 22-AUG-1997; 97US-0056864.  
PR 22-AUG-1997; 97US-0056872.  
PR 22-AUG-1997; 97US-0056874.  
PR 22-AUG-1997; 97US-0056875.  
PR 22-AUG-1997; 97US-0056876.  
PR 22-AUG-1997; 97US-0056877.  
PR 22-AUG-1997; 97US-0056878.  
PR 22-AUG-1997; 97US-0056879.  
PR 22-AUG-1997; 97US-0056880.  
PR 22-AUG-1997; 97US-0056881.  
PR 22-AUG-1997; 97US-0056882.  
PR 22-AUG-1997; 97US-0056884.  
PR 22-AUG-1997; 97US-0056886.  
PR 22-AUG-1997; 97US-0056887.  
PR 22-AUG-1997; 97US-0056888.  
PR 22-AUG-1997; 97US-0056889.  
PR 22-AUG-1997; 97US-0056892.  
PR 22-AUG-1997; 97US-0056893.  
PR 22-AUG-1997; 97US-0056894.  
PR 22-AUG-1997; 97US-0056903.  
PR 22-AUG-1997; 97US-0056908.  
PR 22-AUG-1997; 97US-0056909.  
PR 22-AUG-1997; 97US-0056910.  
PR 22-AUG-1997; 97US-0056911.  
PR 05-SEP-1997; 97US-0056911.  
PR 05-SEP-1997; 97US-0057650.  
PR 05-SEP-1997; 97US-0057669.  
PR 05-SEP-1997; 97US-0057761.  
PR 12-SEP-1997; 97US-0058785.  
(HUMA-) HUMAN GENOME SCI INC.  
PA Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;  
XX Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
PI Ryan H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
XX WPI; 1998-506364/43.  
DR P-PSDB; AAW74818.  
XX  
PT New isolated human genes and the secreted polypeptide(s) they encode  
PT - useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders



PR 22-AUG-1997; 97US-0056664.  
 PR 22-AUG-1997; 97US-0056845.  
 PR 22-AUG-1997; 97US-0056862.  
 PR 22-AUG-1997; 97US-0056862.  
 PR 22-AUG-1997; 97US-0056874.  
 PR 22-AUG-1997; 97US-0056874.  
 PR 22-AUG-1997; 97US-0056875.  
 PR 22-AUG-1997; 97US-0056876.  
 PR 22-AUG-1997; 97US-0056877.  
 PR 22-AUG-1997; 97US-0056878.  
 PR 22-AUG-1997; 97US-0056879.  
 PR 22-AUG-1997; 97US-0056880.  
 PR 22-AUG-1997; 97US-0056881.  
 PR 22-AUG-1997; 97US-0056882.  
 PR 22-AUG-1997; 97US-0056884.  
 PR 22-AUG-1997; 97US-0056886.  
 PR 22-AUG-1997; 97US-0056887.  
 PR 22-AUG-1997; 97US-0056888.  
 PR 22-AUG-1997; 97US-0056889.  
 PR 22-AUG-1997; 97US-0056892.  
 PR 22-AUG-1997; 97US-0056893.  
 PR 22-AUG-1997; 97US-0056894.  
 PR 22-AUG-1997; 97US-0056903.  
 PR 22-AUG-1997; 97US-0056908.  
 PR 22-AUG-1997; 97US-0056909.  
 PR 22-AUG-1997; 97US-0056910.  
 PR 22-AUG-1997; 97US-0056911.  
 PR 05-SEP-1997; 97US-0057650.  
 PR 05-SEP-1997; 97US-0057669.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 12-SEP-1997; 97US-0058785.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.

PI Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA;  
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
 PI Kiyaw H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
 XX  
 DR WPI: 1998-506364/43.  
 DR P-PSDB: AAW74961.

PT New isolated human genes and the secreted polypeptide(s) they encode  
 PT - useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders

XX Claim 1; Page 472; 721pp; English.

XX This sequence represents a nucleic acid molecule designated Gene 88 from  
 CC the human CDNA clone HANV432 (deposited as clone ATCC 97897 and ATCC  
 CC 209043) which encodes a secreted human protein. The gene can be used to  
 CC generate fusion proteins by linking to the gene to a human  
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of  
 CC the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-595812; amino acid sequences AAW74731-W75026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 186  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAV59511 for described uses).

XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;

XX Alignment Scores:

Pred. No.: 9,27e-58 Length: 506  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-801-115B-2 (1-99) x AAV59746 (1-506)

QY 1 MetAspAsnValGlnProlystlelyshsArgProphCysPheSerVallysglyhs 20  
 Db 117 ATGGATTAACGTGACGCGAAATATAACATATGCGCTGCTGAGTGAAGGCCAC 176  
 QY 21 VallyMetleuArgleuaspilleleasenserieValThrThValPheMetleulle 40  
 Db 177 GTCAATATGCTGCGGTGATATATACATCTACGTGTACACAGATATGCTCATTC 236  
 QY 41 ValSerValleuAlaleuileProgluThrThrleuThrValGlyGlyValPhe 60  
 Db 237 GTATCTGTGTGACATGATACAGAAACACACAAATGACAGTTGCTGAGGCTGTT 296  
 QY 61 AlaleuValThrAlaValCysCysleuAlaaspGlyAlaLeuileTyrArgPstleu 80  
 Db 297 GCACCTGTGACACAGATATGCTGTGCGAGGCGGCTTATTTACCGGAAGCTTCTG 356  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValleu 99  
 Db 357 TTCAATCCAGCGGTCTTACAGAAATAGCTGTGCATGAAAAAAGAAAGTTTG 413

RESULT 5  
 ID AAA87730  
 XX AAA87730 standard; cDNA; 515 BP.

AC AAA87730;

DT 28-NOV-2000 (first entry)

DE Human secreted protein encoding cDNA SEQ ID #29.

XX Human: secreted protein; forensic procedure; gene therapy;  
 KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;  
 KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;  
 KW brain disorder; skeletal muscle disorder; eye disorder; obesity;  
 KW mitochondrialcytopathy; diabetes; atherosclerosis; Alzheimer's disease;  
 KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;  
 KW septic shock; impotence; ss.

OS Homo sapiens.

XX WO200037491-A2.

PD 29-JUN-2000.

XX 20-DEC-1999; 99WO-IB02058.

XX 22-DEC-1998; 98US-0113686.

XX 25-JUN-1999; 99US-0141032.

XX (GEST) GENSET.

PI Bougueleret L, Dumas J, Duclert A;

DR WPI: 2000-442637/38.

DR P-PSDB: AAB25768.

PT Polynucleotides and polypeptides encoding proteins with signal  
 PT peptides, useful in diagnostic, forensic, gene therapy and chromosome  
 PT mapping procedures -

PS Claim 1; Page 169-170; 306pp; English.

XX This sequence represents human cDNA encoding a secreted protein. The  
 CC invention relates to sequences AAA87725-AA8774 which encode human  
 CC secreted proteins AAB25763-B25812. The proteins include signal peptides.  
 CC Included in the invention are a host cell containing one of the cDNA  
 CC sequences, and a purified antibody capable of binding to one of the  
 CC secreted proteins. Also contained in the invention are methods for  
 CC storing the sequence data on a computer system, and a method for  
 CC identifying features of the cDNA sequences using a computer programme.

CC The cDNAs are useful for expressing secreted proteins or fragments to  
CC obtain antibodies capable of specifically binding to the secreted  
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene  
CC therapy and chromosome mapping procedures and may be used to design  
CC expression vectors and secretion vectors. The proteins of the invention  
CC may be used to treat diseases including cancer, autoimmune diseases,  
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological  
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye  
CC disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis,  
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,  
CC dementia, hyperlipidaemia, septic shock and impotence.

50 Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment Scores:	
Pred. No.:	9,49e-58
Score:	515
Percent Similarity:	100.00
Best Local Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	21
length:	515
Matches:	99
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-801-115B-2 (1-99) x AAA87730 (1-515)

QY 1 MetAspAsuValGlnProIysIleIySHsAArgProPheCysPheSerValIleGlyHis 20  
Db ATGGATATACGTCGACGCCGAAATATAAACAATCCGCCCTTCGCTTCAGTGAATAAAGGCCAC 203  
144  
QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
Db GTGAATATGCTGGCGCTGATATATATCAACTCAGTGTATACAGAGTATCATGCTATC 263  
204  
QY 41 ValSerValLeuAlaLeuIleProGluThrThrPheLeuThrValGlyGlyValPhe 60  
Db GATTCGTGTGGCACTGATACCAAGAAACCAACAAATTGACAGTGGTGAGGGGTGTT 322  
264  
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspIleAlaLeuIleTyrArgIlysLeu 80  
Db GCACCTGTACAGCAATGATGCTGCTTGGCGCAGGGGCCCTTATATTACGGAAAGCTTCGTG 383  
324  
QY 81 PheAsnProSerGlyProCfrrGlnIlyIysProValHisGluIyIysGluValLeu 99  
Db TTTCATATCCACGGCGTCTTACCAAGAAAAGCCTGGCATGAAAAAAGGAAGTTTGG 440  
384

RESULT 6  
AAAF64012  
ID AAAF64012 standard; cDNA; 515 BP

AC AAF64012;

DT 05-APR-2001 (first entry)

CDNA encoding human secreted protein #13.

**KW** Secreted protein; prevention; treatment; diagnosis; disease; infection; diagnosis

KW Infection; ds.

05 Homo sapien

PN WO200100806-A2

PD 04-JAN-2001.

PF 21-JUN-2000; 2000WO-IB00951.

PR 25-JUN-1999; 99US-0141032.

PR 21-DEC-1999; 99US-0469099.

PA (GEST ) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S,  
...

DR WPI; 2001-071487/08

XX 49 Secreted proteins and the nucleic acids encoding them, useful in  
PT gene therapy and for detecting similar sequences in samples -  
XX  
PS Claim 1; Page 225; 307pp; English.

CC The present invention relates to 49 secreted proteins and the cDNAs  
CC encoding them. The protein and nucleic acids may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate protein expression.

SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment Scores:	
Pred. No.:	9,49e-58
Score:	508.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	22
Length:	515
Matches:	99
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-801-115B-2 (1-99) X AAF64012 (1-515)

OY	MetAspAsnValAlaInProLysIleLysHisAqProPheCysPheSerValLysGlyHis	20
Db	144 ATGGATTAACGTGCAGCCGAAATAATTAACAATGCCCCCTTCTGCTTCAGTGTAAAGGCCAC	203
OY	ValLysMetLeuArgLeuAspIleLeaSerLeuValThrThrValPheMetLeuIle	40
Db	204 GTGAACATGCGCGCGCTGATATTATTAACAATCACTCAGTAAACAGATTCATCTCATC	263
OY	ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe	60
Db	264 GTATCTGTGTGGCACTGATTACCAAGAACACAAATTGACAGTTGGTGGAGGGGTGTTT	322
OY	AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu	80
Db	324 GCACCTGTGCACAGCACTATGCTGCTTCGCCGACGGGGCCCTTAATTACCGGAACCTCTG	383
OY	PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu	99
Db	384 TTCAATCCCAAGCGGCTCTTACCAAGAAAAGCGCTGTGCATGAATAAAAAGAAGTTTGG	440

RESULT 7  
AAA38006  
ID AAA38006 standard; cDNA; 534 BP

AC AAA38006;

DT 22-AUG-2000 (first entry)

UCK-1 nucleotide sequence.

KW UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;

kw radiotherapy; chemotherapy; human; ss: 100

OS Homo sapiens.

PN CN1244584-A.

PD 16-FEB-2000.

PF 14-MAY-1999; 99CN-0107284-  
 YY

PR 14-MAY-1999; 99CN-0107284.

PA (UYBE-) UNIV BEIJING MEDICAL  
XX

PI Ma D, Han W, Zhang Y;

DR WPI; 2000-388170/34.

XX

PT Chemotactic factor useful for treatment and diagnosis of immunocyte  
PT disorders - has immunocyte chemotactic stimulating factor  
XX  
XX  
PS Example 4; Fig 1; 31pp; Chinese.  
CC This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis  
CC factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis  
CC activity and a haemopoiesis stimulating effect. The invention relates to  
CC UCK proteins, their encoding nucleotide sequences and antibodies and  
CC antagonists against the proteins. The nucleotide and protein sequences  
CC are useful for the preparation of a composition for the diagnosis and  
CC treatment of diseases associated with abnormal immunocyte function and  
CC low haemopoiesis function caused by radiotherapy and chemotherapy used to  
CC treat tumours and other diseases.  
XX  
SQ Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 9.97e-58 Length: 534  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
  
US-09-801-115B-2 (1-99) x AAA38006 (1-534)  
QY 1 MetaspasnaValGlnProlysiLeuLysHisArgProheCysPheSerVallysglyHis 20  
Db 152 ATGATTAACGTGCGACGCGGAAATAAACATCGCCCTTCGCTTCACTGTAAGGCCAC 211  
QY 21 VallysmetleuArgleuAspIlelleAsnSerleuValThrThrValPheMetleu 40  
Db 212 GTGAAGATGCGCGCGGATATTCATCACTGATGTAACACAGATTCATGCTATC 271  
QY 41 ValserValleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
Db 272 GTACTGTGTGGACATGATACCAAGAAACCAACATGACAGTGGAGGGGTGTT 331  
QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArglyLeu 80  
Db 332 GCACCTGTGACACAGATGCTGCTTGGCCGAGGGGCCCTTATTTACCGAGACTCTG 391  
QY 81 PheAsnProSerGlyProTyrrGlnLysLysProValHisGluLysGluValLeu 99  
Db 392 TTCATGCCACGCGCTTACCAGAAAAGCGCTGATGTAAGAAAAGAGTTTGG 448  
  
RESULT 8  
AAH98515/c  
ID AAH98515 standard; cDNA: 538 BP.  
AC AAH98515;  
XX  
DT 12-OCT-2001 (first entry)  
DE Human EST-derived coding sequence SEQ ID NO: 372.  
XX  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition; ss.  
OS Homo sapiens.  
XX  
XX MO200154477-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02687.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
XX 17-JUL-2000; 2000US-0617746.  
XX 03-AUG-2000; 2000US-0631451.  
XX

PR 15-SEP-2000; 2000US-0663870.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Dymnac RA, Zhang J, Werhman T;  
XX  
XX WPI: 2001-476164/51.  
DR P-PsDB; AAM23856.  
XX  
XX  
PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use -  
XX  
XX Claim 1; Page 451; 1275pp; English.  
CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention.  
XX  
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.01e-57 Length: 538  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
  
US-09-801-115B-2 (1-99) x AAH98515 (1-538)  
QY 1 MetaspasnaValGlnProlysiLeuLysHisArgProheCysPheSerVallysglyHis 20  
Db 366 ATGATTAACGTGCGACGCGGAAATAAACATCGCCCTTCGCTTCACTGTAAGGCCAC 307  
QY 21 VallysmetleuArgleuAspIlelleAsnSerleuValThrThrValPheMetleu 40  
Db 306 GTGAAGATGCGCGCGGATATTCATCACTGATGTAACACAGATTCATGCTATC 247  
QY 41 ValserValleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
Db 246 GTACTGTGTGGACATGATACCAAGAAACCAACATGACAGTGGAGGGGTGTT 187  
QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrArglyLeu 80  
Db 186 GCACCTGTGACACAGATGCTGCTTGGCCGAGGGGCCCTTATTTACCGAGACTCTG 127  
QY 81 PheAsnProSerGlyProTyrrGlnLysLysProValHisGluLysGluValLeu 99  
Db 126 TTCATGCCACGCGCTTACCAGAAAAGCGCTGATGTAAGAAAAGAGTTTGG 70  
  
RESULT 9  
AAH98548/c  
ID AAH98548 standard; cDNA: 538 BP.  
AC AAH98548;  
XX  
DT 12-OCT-2001 (first entry)  
DE Human EST-derived coding sequence SEQ ID NO: 405.  
XX  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition; ss.  
OS Homo sapiens.  
XX

PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001: 2001WO-US02687.  
 XX  
 PR 25-JAN-2000: 2000US-0491404.  
 PR 17-JUL-2000: 2000US-0617746.  
 PR 03-AUG-2000: 2000US-0631451.  
 PR 15-SEP-2000: 2000US-0663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 DR WPI: 2001-476164/51.  
 DR P-PSDB: AAM23889.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1: Page 467; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.01e-57 Length: 538  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-801-115B-2 (1-99) x AAH98548 (1-538)  
 QY 1 MetaspasValaGlnProlySilelySHsArGProPhCySPhSeVallysglyHis 20  
 DB 366 ATGGATTAACGTGACAGCCGAAATTAACATCCCTCTGCTTCAAGTGAAGGCCAC 307  
 QY 21 VallySMetLeuArGLeuAspIleleAsnSerLeuValThrThrValPheMetLeuIle 40  
 DB 306 GTGAAGATGCTCGCGCTGATATATCAACTACACGTAAACAACAGTATTCATGCTCATC 247  
 QY 41 ValSerValleuAlaLeuIleProGluThrThrThrThrValAlglyGlyValPhe 60  
 DB 246 GATATCTGTTGGCAGCTGATACCAACCAACCAATTGACAGATTGGTGGAGGGGTTT 187  
 QY 61 AlaleuValThralaValaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 DB 186 GCATCTGTGACAGCAGTATGCTGCTCCGACGGGGCCCTATTATTCGGAAGCTTCTG 127  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValleu 99  
 DB 126 TTCATCCACAGGGGCTCTTACAGAGAAAAAGCCGTGATGAAAAAAGAGTTTGTG 70  
 RESULT 10  
 AAH34835  
 ID AAH34835 standard; cDNA, 558 BP.  
 XX  
 AC AAH34835;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX

DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.  
 XX  
 KM Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KM colorectal carcinoma; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200122920-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 28-SEP-2000: 2000WO-US26524.  
 XX  
 PR 29-SEP-1999: 99US-0157137.  
 PR 03-NOV-1999: 99US-0163280.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
 PI WPI: 2001-235357/24.  
 DR P-PSDB: AAG75430.  
 DR  
 DR  
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX  
 PS Claim 1: Page 3428; 9803pp; English.  
 XX  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patients own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated Ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAB77789 represent sequences used in the exemplification of the  
 CC present invention.  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.06e-57 Length: 558  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-801-115B-2 (1-99) x AAH34835 (1-558)  
 QY 1 MetaspasValaGlnProlySilelySHsArGProPhCySPhSeVallysglyHis 20  
 DB 147 ATGGATTAACGTGACAGCCGAAATTAACATCCCTCTGCTTCAAGTGAAGGCCAC 206  
 QY 21 VallySMetLeuArGLeuAspIleleAsnSerLeuValThrThrValPheMetLeuIle 40  
 DB 207 GTGAAGATGCTCGCGCTGATATATCAACTACACGTAAACAACATATTCATGCTCATC 266  
 QY 41 ValSerValleuAlaLeuIleProGluThrThrThrThrValAlglyGlyValPhe 60  
 DB 267 GATATCTGTTGGCAGCTGATACCAACCAACCAATTGACAGATTGGTGGAGGGGTTT 326  
 QY 61 AlaleuValThralaValaCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80



DB 327 GCACCTGTGACAGACGATGCTGTGCGACGGGCGCTTATTAACGGAAGCTCTG 386  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 DB 387 TTCATGCCAGCGGCTCTTACCAAGAAAAAGCTGTGATGAAAAAAGAGTTTG 443  
 RESULT 11  
 ID AAS44932 standard; cDNA; 655 BP.  
 AC AAS44932;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE cDNA encoding novel human secretory protein, Seq ID No 13.  
 XX  
 KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;  
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200166689-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PE 05-MAR-2001; 2001WO-US04942.  
 XX  
 PR 07-MAR-2000; 2000US-0519705.  
 PR 19-MAY-2000; 2000US-0574454.  
 PR 17-JUN-2000; 2000US-0596193.  
 PR 14-JUL-2000; 2000US-0616847.  
 PR 19-SEP-2000; 2000US-0665363.  
 PR 20-OCT-2000; 2000US-0693267.  
 XX  
 PA (HXSE-) HXSEQ INC.  
 XX  
 PI Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;  
 PI Zhao QH, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;  
 XX  
 DR WPI: 2001-589934/66.  
 DR P-PSDB: AAU28032.  
 XX  
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries  
 PT prepared from various human tissues, for diagnosis and treatment of  
 PT cancer, neurological, inflammatory, and autoimmune disorders -  
 XX  
 XX  
 PS Claim 1; SEQ ID No 13; 107bp; English.  
 XX  
 CC The invention relates to novel isolated human secreted polypeptides (I)  
 CC and polynucleotides (II). (I) and (II) are useful for treating  
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,  
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is  
 CC involved in increasing haematopoiesis, stem cell survival, bone growth  
 CC and remodeling. (I), (II) and modulators of (II) are useful for  
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for  
 CC creating transgenic animals useful for studying the in vivo activities of  
 CC the polypeptide as well as for studying modulators of the polypeptides.  
 CC (I) induces the proliferation of neural cells and regeneration of nerve  
 CC and brain tissue and is useful for the treatment of central and  
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,  
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral  
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic  
 CC activity, regulation of haematopoiesis and is useful for treating myeloid  
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia  
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve

CC tissue growth, and in tissue repair, healing of burns, incisions,  
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative  
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for  
 CC gut protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, various immune deficiencies and  
 CC disorders including severe combined immunodeficiency (SCID), bacterial or  
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,  
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic  
 CC reactions and conditions, such as asthma or other respiratory problems.  
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,  
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of  
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides  
 CC analgesic effects or other pain reducing effects, immunoglobulin like  
 CC activity and can act as an antigen in a vaccine composition to raise an  
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein  
 CC coding sequences of the invention.  
 XX  
 SQ Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,31e-57 Length: 655  
 Score: 508.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 XX  
 US-09-801-115B-2 (1-99) \* AAS44932 (1-655)  
 QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGluHis 20  
 DB 134 ATGATATACGTGACGCGAATAATAAACATCCGCCCTTCCTGCTGATGTAAGGCCAC 193  
 QY 21 ValLysMetLeuArgLeuAspIleLeaSerLeuValThrThrValPheMetLeuLeu 40  
 DB 194 GTGAAATGCTGCGGCTGCGATATTATCACTACGTGTAACAACAGTATTCCTCATC 253  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 DB 254 GTATCTGTGTGGACATGATACCAAGAACACAACTTGACAGTGTGGAGCGGTGTTT 313  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80  
 DB 314 GCACCTGTGACACAGATATGCTGTGGCGACGGGCGCTTATTTACCGGAAGCTCTG 373  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 DB 374 TTCATGCCAGCGGCTCTTACCAAGAAAAAGCTGTGATGAAAAAAGAGTTTG 430  
 RESULT 12  
 ID AAL15919 standard; cDNA; 297 BP.  
 AC AAL15919;  
 XX  
 DT 12-JUN-2000 (first entry)  
 XX  
 DE Human protein clone HP10357 coding sequence.  
 XX  
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;  
 KW cytokine production; cell proliferation; cell differentiation;  
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;  
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;  
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;  
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;  
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;  
 KW coagulation disorder; myocardial infarction; inflammatory condition;  
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;  
 XX  
 OS Homo sapiens.  
 XX

PN WO200005367-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 22-JUL-1999; 99WO-JP03929.  
 XX  
 PR 24-JUL-1998; 98JP-0208820.  
 PR 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 PR 29-SEP-1998; 98JP-0275505.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 PI Kato S, Kimura T;  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: AAY94861.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 XX  
 PS Claim 3; Page 217-218; 351pp; English.  
 XX  
 CC This sequence encodes a human protein of the invention, which has  
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a  
 CC genetic marker. The protein can also be used as a marker, and to identify  
 CC potential genetic disorders. The DNA and protein can also be used as  
 CC nutritional sources or supplements. The protein exhibits cytokine, cell  
 CC proliferation, cell differentiation activities and induces production of  
 CC immune stimulating or immune suppressing activity. It can be used in the  
 CC treatment of various immune deficiencies and disorders, and to treat  
 CC infectious diseases caused by viral, bacterial, fungal or other  
 CC infections. The protein is also used for treating autoimmune disorders  
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid  
 CC arthritis. It is also useful in the treatment of allergic reactions and  
 CC conditions such as asthma, and in immune suppression after organ  
 CC transplantation. The protein is useful in regulation of haematopoiesis  
 CC and consequently in the treatment of myeloid or lymphoid cell  
 CC deficiencies. It is also used in compositions for tissue growth or  
 CC regeneration. The protein is also used in the treatment of osteoporosis  
 CC or osteoarthritis and in the treatment of periodontal disease and other  
 CC tooth repair processes. The protein is used in the treatment of nervous  
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and  
 CC Huntington's disease. They are useful for protection or regeneration and  
 CC treatment of lung or liver fibrosis, reperfusion injury in various  
 CC tissues, and conditions resulting from systemic cytokine damage. They are  
 CC also used for promoting or inhibiting tissue differentiation. They are  
 CC also used as contraceptives since they exhibit activin or inhibin related  
 CC activities and as a fertility inducing therapeutic. They are used for  
 CC treating various coagulation disorders and in treatment and prevention of  
 CC conditions resulting from coagulation activities e.g. myocardial  
 CC infarction or stroke. They also acts as receptors, receptor ligands or  
 CC inhibitors or agonists of receptor/ligand interactions. They are used to  
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia  
 CC reperfusion injury, arthritis, and nephritis. They can be used to  
 CC prevent tumours.  
 XX  
 SQ Sequence 297 BP; 81 A; 68 C; 72 G; 76 T; 0 other:

## Alignment Scores:

Pred. No.: 1.52e-57 Length: 297  
 Score: 504.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 98.99% Mismatches: 0  
 Query Match: 99.21% Gaps: 0  
 DB: 21

US-09-801-115B-2 (1-99) x AAY15919 (1-297)

QY 1 MetaspasnaValGlnProLysIleLysHISArgProPheserValLysGlyHis 20  
 DB 1 ATGGATTAAGCTGACGCCGAAATATAACATCGCCCTTCTGCTGCTGAGTGAAGGCCAC 60  
 QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40  
 DB 61 GTGAAAGATGCTGGCGGCTGGATATTATCAACTCACTGTAACACACTATTTCATGCTCANC 120  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 DB 121 GTATCTGTGTGGCAGTACGATACCAAGAACCAATATACAGTTGTGGAGGGGTGT 180  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 DB 181 GCACCTGTGACACAGATATCTGTCTTCCGACGGGGCCCTTATTACCGAAGCTTCG 240  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99  
 DB 241 TTCAATCCAGCGCTGCTTACACGAAAGCCGTGTCATGAAAAAAGAAAGTTTGG 297  
 RESULT 13  
 ID AAY15929 standard; cDNA; 467 BP.  
 XX  
 AC AAY15929;  
 XX  
 DE 12-JUN-2000 (first entry)  
 XX  
 XX Human protein clone HP10357 full length coding sequence.  
 KW Human protein; hydrophobic domain; nutritional source; haematopoiesis;  
 KW cytokine production; cell proliferation; cell differentiation;  
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;  
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;  
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;  
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;  
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;  
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;  
 KW coagulation disorder; myocardial infarction; inflammatory condition;  
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;  
 KW nephritis; therapy; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200005367-A2.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 22-JUL-1999; 99WO-JP03929.  
 XX  
 PR 24-JUL-1998; 98JP-0208820.  
 PR 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 PR 29-SEP-1998; 98JP-0275505.  
 XX  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 PI Kato S, Kimura T;  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: AAY94861.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 XX  
 PS Claim 4; Page 228; 351pp; English.  
 XX  
 CC This sequence encodes a human protein of the invention, which has  
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a  
 CC genetic marker. The protein can also be used as a marker, and to identify



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XX AAA38007;
AC
XX 22-AUG-2000 (first entry)
DT
XX UCK-2 nucleotide sequence.
DE
XX UCK-2; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
KM radiotherapy; chemotherapy; human; ss.
XX
XX Homo sapiens.
OS
XX CN1244584-A.
PN
XX 16-FEB-2000.
PD
XX 14-MAY-1999; 99CN-0107284.
PE
XX 14-MAY-1999; 99CN-0107284.
PR
XX (UYBE-) UNIV BEIJING MEDICAL.
PA
XX Ma D, Han W, Zhang Y;
PI
XX WPI; 2000-388170/34.
DR
XX P-PSDB; AAY98143.
DR
XX Chemotactic factor useful for treatment and diagnosis of immunocyte
PT disorders - has immunocyte chemotactic stimulating factor
PS
XX Example 4; Fig 2; 31pp; Chinese.
PS
XX This sequence represents an UCK-2 cDNA sequence encoding a chemotaxis
CC factor polypeptide. The UCK-2 protein exhibits immunocyte chemotaxis
CC activity and a haemopoiesis stimulating effect. The invention relates to
CC UCK proteins, their encoding nucleotide sequences and antibodies and
CC antagonists against the proteins. The nucleotide and protein sequences
CC are useful for the preparation of a composition for the diagnosis and
CC treatment of diseases associated with abnormal immunocyte function and
CC low haemopoiesis function caused by radiotherapy and chemotherapy used to
CC treat tumours and other diseases.
CC
XX
XX SQ Sequence 459 BP; 123 A; 99 C; 96 G; 141 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 5,43e-53 Length: 459
XX Score: 471.50 Matches: 99
XX Percent Similarity: 65.138 Conservative: 0
XX Best Local Similarity: 65.138 Mismatches: 0
XX Query Match: 92.814 Indels: 53
XX DB: 21 Gaps: 1
XX
XX US-09-801-115b-2 (1-99) x AAA38007 (1-459)
XX
QY 1 MetASPasnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 1 ATGGATAAACGTCAGCGCAAAATAAACAATCGCCCTTCTGCTCAGTGTGAAGCCAC 60
QY 21 ValLysMetLeuArg----- 25
DB 61 GTGAGATCTGCGCTGCGCACTAACTGTGACATCTAGACCTTTTATCATCGCACAA 120
QY 25 ----- 25
DB 121 GCCCGTGAACCATATATTTGTATCATGATTTGAAGTCACCGGTATCTATTTTCATA 180
QY 26 -----Leuasp 27
DB 181 CTTTATATGTAAGTATGATGATTAATGAAGTGTATTTTGCCCTTGCTGAT 240
QY 28 IleIleAsnSerLeuValThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
DB 241 ATTATCACTCACTGGTAAACAGATATTCATGCTATCTGTGTGGCACTGATA 300

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QY 48 ProGlnThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
DB 301 CCAGAAACACACACATTTGACAGTTGTGAGGGGTGTTTGCACCTTGTGACAGCATATGC 360
QY 68 CysLeuAlaAspGlyAlaLeuIleTyPArgLysLeuLeuPheAsnProSerGlyProTy 87
DB 361 TGTCTTGGCCGACGGGGCCCTTATTTACGGAGGCTTCTGTCAATCCACAGGCTCCTAC 420
QY 88 GlnLysLysProValHisGlnLysLysGlnValLeu 99
DB 421 CAGAAAAAGCCTGTGATGAAAAAAGAAAGTTTG 456

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Search completed: June 25, 2003, 12:51:07  
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GenCore version 5.1.6  
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Run on: June 25, 2003, 12:33:06 ; Search time 65 seconds  
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467.092 Million cell updates/sec

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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCrUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	508	100.0	504	US-09-149-476-98	Sequence 98, Appl
2	508	100.0	506	US-09-149-476-252	Sequence 252, App
3	357	70.3	392	US-09-385-982-95	Sequence 95, Appl
4	83	16.3	37948	US-09-251-645-11	Sequence 11, Appl
5	73	14.4	1083	US-09-116-498-11	Sequence 11, Appl
6	71	14.0	1083	US-09-116-498-7	Sequence 7, Appl
7	66.5	13.1	720	US-08-061-092A-2	Sequence 2, Appl
8	66	13.0	4403765	US-09-103-840A-2	Sequence 2, Appl
9	66	13.0	4411529	US-09-103-840A-1	Sequence 1, Appl
10	65.5	12.9	43676	US-09-356-952-12	Sequence 12, Appl
11	65	12.8	3872	US-09-165-386-1	Sequence 1, Appl
12	64.5	12.7	1333	US-08-684-862-9	Sequence 9, Appl

13	64.5	12.7	2211	4	US-09-462-844-1	Sequence 1, Appl
14	64.5	12.7	7721	3	US-08-772-270A-14	Sequence 14, Appl
15	64	12.6	17710	4	US-08-976-259-70	Sequence 70, Appl
16	64	12.6	25165	4	US-09-453-702B-39	Sequence 39, Appl
17	63.5	12.5	654	4	US-08-898-416-176	Sequence 176, App
18	63.5	12.5	1785	4	US-09-377-135-8	Sequence 8, Appl
19	63.5	12.5	1785	4	US-09-669-974-6	Sequence 6, Appl
20	63.5	12.5	2153	4	US-09-367-206-6	Sequence 6, Appl
21	63	12.4	1854	1	US-08-249-420-1	Sequence 1, Appl
22	63	12.4	1854	2	US-08-737-663-1	Sequence 1, Appl
23	63	12.4	4403765	4	US-09-103-840A-2	Sequence 2, Appl
24	63	12.4	4411529	4	US-09-103-840A-1	Sequence 1, Appl
25	62.5	12.3	615	4	US-09-134-001C-376	Sequence 376, App
26	62.5	12.3	1105	4	US-09-221-017B-108	Sequence 108, App
27	62.5	12.3	9711	4	US-08-961-527-167	Sequence 167, App
28	62	12.2	745	4	US-09-221-017B-319	Sequence 319, App
29	62	12.2	819	1	US-08-309-182B-2	Sequence 2, Appl
30	62	12.2	6943	4	US-09-453-702B-213	Sequence 213, App
31	61.5	12.1	1327	6	US-08-878-989-14	Sequence 14, Appl
32	61.5	12.1	1435	2	US-08-878-989-14	Sequence 14, Appl
33	61.5	12.1	1435	4	US-09-272-796-14	Sequence 14, Appl
34	61.5	12.1	3706	4	US-08-913-159-9	Sequence 9, Appl
35	61.5	12.1	3725	1	US-08-155-331-12	Sequence 12, Appl
36	61.5	12.1	3725	1	US-08-424-022-12	Sequence 12, Appl
37	61.5	12.1	3725	2	US-08-424-017B-12	Sequence 12, Appl
38	61.5	12.1	3725	5	PCr-US93-11696-12	Sequence 12, Appl
39	61	12.0	1083	4	US-09-116-498-9	Sequence 9, Appl
40	61	12.0	8396	4	US-09-328-174A-1	Sequence 1, Appl
41	61	12.0	8409	4	US-09-167-681-37	Sequence 37, Appl
42	61	12.0	13417	2	US-08-637-739B-37	Sequence 37, Appl
43	61	12.0	13417	3	US-08-871-355A-37	Sequence 37, Appl
44	61	12.0	13417	4	US-09-201-945-37	Sequence 37, Appl
45	61	12.0	61663	4	US-09-453-702B-62	Sequence 62, Appl

## ALIGNMENTS

RESULT 1  
US-09-149-476-98  
Sequence 98, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
EARLIER FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23

[illegible][illegible]

EARLIER APPLICATION NUMBER: 60/056, 875  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/056, 887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056, 908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048, 964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057, 650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056, 884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057, 669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049, 610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061, 060  
EARLIER FILING DATE: 1997-10-02

## Alignment Scores:

Pred. No.:	2,43e-66	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-801-115b-2 (1-99) x US-09-149-476-98 (1-504)

QY 1 MetaspsnValGlnProLysIleLysHisArgProPheCysPheSerVallysgLysIle 20  
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QY 21 VallysmeLueArlgleuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40  
DB 191 GTGAAGATGCTGCGCGTGATATTATCACTCACTGTACACAGATTCATCATCTCATC 250  
QY 41 ValserValleuAlaLeuIleProGluThrThrLeuThrValIleGlyGlyValPhe 60  
DB 251 GATCTGTGTGGCGCGTATTCAGAAACCAACCATTTGAGTGTGGGGGTGTTT 310  
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspIleValLeuIleTyrArgLysLeu 80  
DB 311 GCACCTGTGACAGACAGATGCTGTCTGCGCAGCGGCCCTTATTACCGAAGCTCTG 370  
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValLeu 99  
DB 371 TTCAATCCACGCGGTCTTACAGAAAAAGCCTGTGATGAAAAAAGAAATTTTG 427

## RESULT 2

US-09-149-476-252

Sequence 252, Application US/09149476

Patent No. 6420526

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149, 476

EARLIER FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040, 162

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 333

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038, 621

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 626

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040, 336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047, 600  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 502  
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EARLIER APPLICATION NUMBER: 60/043, 569  
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EARLIER APPLICATION NUMBER: 60/048, 974



EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
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EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
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EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Alignment Scores:  
Pred. No.: 2,44e-66 Length: 506  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-801-115b-2 (1-99) x US-09-149-476-252 (1-506)

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Db 117 ATGGATACGTCGCGCGGAAATAAACATCGCCCTTCGCTTCAGTGGAAGGCCAC 176  
21 Valysmetleuargleuasp1leleasnserleuvalthrvalphemetleuile 40  
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Db 177 GTGAAGATGTCGCGCGCGATATATCACTACGTGTAAACAACATATTCATGCTCATC 236  
41 valservalleualaleuileplogluhrth-thleuthrvalajlyglyvalphe 60  
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Db 237 GTATCTGTGTTCGACATGATCCAGAACCAACATTCACATTTGTGTGAGGGGTGTT 296  
Qy 61 Alaleuvalthrvalayalyscysleualasp1alaleuilethrargylsleu 80  
|||||  
Db 297 GCACCTGTGACAGAGATGCTGCTTGGCGACGGGGCCCTTATTTACCGGAAGCTTCG 356  
Qy 81 Pheasnproserglyprotyrglnlyslsprovahisglulysgluvalleu 99  
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Db 357 TTCATGCCAGCGGCTTCCTTACGAAAGAGCCGTGCTCATGAAGAAAGACTTTG 413

RESULT 3

US-09-385-982-95  
Sequence 95, Application US/09385982  
Patent No. 6262334

GENERAL INFORMATION:

APPLICANT: ENDREGE, WILSON O., ET AL.  
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
PRODUCTS: II



COMPUTER READABLE FORM:

...

TITLE OF INVENTION: ANTI-CDR-2 ANTIBODIES, COMBINATIONS  
 TITLE OF INVENTION: THEREOF, AND THERAPEUTIC USES THEREOF  
 NUMBER OF INVENTION: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Burns, Doane, Swecker & Mathis  
 STREET: George Mason Bldg., Washington & Prince Sts.  
 CITY: Alexandria  
 STATE: Virginia

```

COUNTRY: United States
ZIP: 22133-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061,092A
FILING DATE: 14-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 018797-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..720
US-08-061-092A-2

Alignment Scores:
Pred. No.: 1.51 Length: 720
Score: 66.50 Matches: 22
Percent Similarity: 48.61% Conservative: 13
Best Local Similarity: 30.56% Mismatches: 20
Query Match: 13.09% Indels: 17
DB: 1 Gaps: 4

US-09-801-115B-2 (1-99) x US-08-061-092A-2 (1-720)

QY 28 llellaasnserleuvalthrvalphemetleullevalservalleu----- 44
Db 684 GTAGTACATAGTACTAGTACATAGTATAGTATAGACACATATAGACGGCAGT 625
QY 45 Alaleulleproslurthrthrleuthrvalgly-----glylyalphealaleu 62
Db 624 GTCTCAGATGTCAGCTGCTGAGCTGAGGTAGGCGCGGTTGAGAGA----- 577
QY 63 valthrAlaValCysCysleualaaspGlyAlaLeuiletyrArglys----- 78
Db 576 -----TGTGTCTGCTGTATTACTGGCCTTGCCCTGGAAATTGCGGTCAATATACAGTATT 523
QY 79 -----leuleupheasnproserglyprotyrGln 88
Db 522 ACCATTCTCAGATGATCATCATCATTCATTCAG 487

RESULT 8
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2

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```

LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 5.03e+05 Length: 4403765
Score: 66.00 Matches: 26
Percent Similarity: 44.57% Conservative: 15
Best Local Similarity: 28.26% Mismatches: 39
Query Match: 12.99% Indels: 12
DB: 4 Gaps: 4

US-09-801-115B-2 (1-99) x US-09-103-840A-2 (1-4403765)

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Db 1499197 GTGGCCGAGCTGTGGCCAGCCAGGTGTGCGCCGTCGCAACAGCAGCTATTGACC----- 1499144
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Db 1499143 -----TGGCAGACGCTGACATGCGCGGCTGTTGACCGCAGATGCGCAGCATGGGCG 1499090
QY 68 CysleualaaspGlyAlaLeuiletyrArglysleuupheasnproserglyProtyr 87
Db 1499089 CTGACTGCAGACAGCGCC-----TGGCGTGGCTG-----GACGTGGGCTGCGCTTTC 1499042
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RESULT 9
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37RV
US-09-103-840A-1

Alignment Scores:
Pred. No.: 5.04e+05 Length: 4411529
Score: 66.00 Matches: 26
Percent Similarity: 44.57% Conservative: 15
Best Local Similarity: 28.26% Mismatches: 39
Query Match: 12.99% Indels: 12
DB: 4 Gaps: 4

US-09-801-115B-2 (1-99) x US-09-103-840A-1 (1-4411529)

QY 8 llelyshlsarprophecyspheserVallysllyshlyVallysmetleuArgleuasp 27

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Pred. No.: 101  
 Score: 64.50  
 Percent Similarity: 39.60%  
 Best Local Similarity: 22.77%  
 Query Match: 12.70%  
 DB: 3  
 Length: 7721  
 Matches: 23  
 Conservative: 17  
 Mismatches: 30  
 Indels: 31  
 Gaps: 4

US-09-801-115B-2 (1-99) x US-08-772-270A-14 (1-7721)

QY 22 LysMetLeuArgLeuAspIleIleAsnSer-----LeuValThr 34  
 DB 7519 CGTCTCTAGACCTTCAATAGATGCTCTTAATGACGACGAGTAAGAACTGATTAACA  
 QY 35 ThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 52  
 DB 7459 CCGCGTTCTCCGTTTATTTCTGCAATACGCTCATTCGAAACCAATGATTTCT 7400  
 QY 53 LeuThrValGlyGlyValPheAlaLeuValThrAlaVal----- 66  
 DB 7399 TTATCACCATCTGTAAATGTTTTCTGTAATCTCAATATGAAATGAAATGAACTAAACCA  
 QY 67 -----CysCysLeuAlaAspGlyAlaLeuIleTyrArg----- 77  
 DB 7339 AGCTGAGGTGCTCAATACATCAAGAGTAATAGTTTACTTTCATAGAGATAACCA 7280  
 QY 78 -----LysLeuLeuPheAsnProSerGlyProTyrGlnLysLys 90  
 DB 7279 TATCTTGTGTAGGAAAGTTTCCACTTAATTAATGCTGCTCTGCAATTTCAACAAAA 7220  
 QY 91 Pro 91  
 DB 7219 CCA 7217

# RESULT 15

US-08-976-259-70  
 ; Sequence 70, Application US/08976259  
 ; Patent No. 6316609

## GENERAL INFORMATION:

APPLICANT: Dillon, Patrick J.  
 APPLICANT: Choi, Gil H.  
 APPLICANT: Welch, Rodney A.  
 TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli  
 Patent No. 6316609

## NUMBER OF SEQUENCES: 142

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
 STREET: 1100 New York Ave, N.W., Suite 600  
 CITY: Washington  
 STATE: DC

## COUNTRY: USA

## ZIP: 20005-3934

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

## COMPUTER: HP Vectra 486/33

## OPERATING SYSTEM: MSDOS version 6.2

## SOFTWARE: ASCII text

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,259

## FILING DATE: Herewith

## CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,626 AND US 60/061,953

## ATTORNEY/AGENT INFORMATION:

NAME: Steife, Eric K.

## REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.074002/EKS/CBM

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 70:

## SEQUENCE CHARACTERISTICS:

LENGTH: 17710 base pairs

TYPE: nucleic acid

STRANDEDNESS: double  
 TOPOLOGY: linear  
 US-08-976-259-70

## Alignment Scores:

Pred. No.: 412  
 Score: 64.00  
 Percent Similarity: 44.00%  
 Best Local Similarity: 25.00%  
 Query Match: 12.60%  
 DB: 4  
 Length: 17710  
 Matches: 25  
 Conservative: 19  
 Mismatches: 40  
 Indels: 16  
 Gaps: 3

US-09-801-115B-2 (1-99) x US-08-976-259-70 (1-17710)

QY 4 ValGlnProLysIleLysHisArgProPheCysPheSerVal----- 17  
 DB 17166 GTTCAGGGTATGCTGAAGCATATGATTTTCCAGCGCCGACGCTGCCGAGCGG 17225  
 QY 18 -----LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSer 31  
 DB 17226 CTTCAGAAAGGAGCGGCTGCAGGAAATATCAGTGCCTGAACAAAGTATGAAGGGGTG 17285  
 QY 32 LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 51  
 DB 17286 CTGGTACATCTCTGCGACCTGGTAGCTGTACAAACGCGCCCTGACATGATCAAAATGTTG 17345  
 QY 52 ThrLeuThrValGlyGlyValPheAla-----LeuValThrAlaValCysCysLeu 69  
 DB 17346 CGGGAGGAGATCTCCGGTGGCGAGTTTCATGAGAAATTTCCGTCGATCTCTGTG 17405  
 QY 70 AlaAspGlyAlaLeu-----IleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87  
 DB 17406 GCAGGTGTGTCTGCGGGTCACTGGCGGGGATATGTTTCAGTCCACTGGGACCATTT 17465

Search completed: June 25, 2003, 13:33:51  
 Job time : 1226 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 13:13:19 ; Search time 135 Seconds

(without alignments)  
1076.113 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508

Sequence: 1 MDVQPKIKHRPFCFSYKGVH.....LFPNSGPYKQPKVHERKEVL 99

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1042519 segs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlp  
-DB=/cgn2.1/USPFO.spool/US09801115/runat\_20062003\_141105\_13685/app\_query.fasta.1.263  
-DB-PUBLISHED=Applications\_NA\_QFMT-fastcap -SUFFIX=rnpb -WINMATCH=0.1  
-LOOPEXT=0 -UNITs-bits -START=1 -END=1 -MATRIX=blomsun62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09801115@cgn.1.1.80 @runat\_20062003\_141105\_13685  
-NCPU=6 -ICU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSHLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:\*

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2: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
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5: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	422	9	US-09-918-995-6534
2	508	100.0	439	9	US-09-823-846-397
3	508	100.0	504	9	US-09-809-391-98
4	508	100.0	506	9	US-09-809-391-252

5	508	100.0	534	10	US-09-801-115-1	Sequence 1, Appl1
6	508	100.0	558	9	US-10-106-698-1927	Sequence 1927, Ap
7	502	98.8	512	9	US-09-918-995-19489	Sequence 19489, A
8	471.5	92.8	459	10	US-09-801-115-3	Sequence 3, Appl1
9	471.5	92.8	663	9	US-09-978-295A-189	Sequence 189, App
10	471.5	92.8	663	9	US-09-978-697-189	Sequence 189, App
11	471.5	92.8	663	9	US-09-978-192A-189	Sequence 189, App
12	471.5	92.8	663	9	US-09-999-832A-189	Sequence 189, App
13	471.5	92.8	663	9	US-09-978-189-189	Sequence 189, App
14	471.5	92.8	663	9	US-09-978-608A-189	Sequence 189, App
15	471.5	92.8	663	9	US-09-978-191A-189	Sequence 189, App
16	471.5	92.8	663	9	US-09-978-403A-189	Sequence 189, App
17	471.5	92.8	663	9	US-09-978-564A-189	Sequence 189, App
18	471.5	92.8	663	9	US-09-978-585A-189	Sequence 189, App
19	471.5	92.8	663	9	US-10-017-081A-189	Sequence 189, App
20	471.5	92.8	663	9	US-09-978-824-189	Sequence 189, App
21	471.5	92.8	663	9	US-09-981-915A-189	Sequence 189, App
22	471.5	92.8	663	9	US-09-999-833A-189	Sequence 189, App
23	471.5	92.8	663	9	US-10-167-749-189	Sequence 189, App
24	471.5	92.8	663	9	US-09-918-585A-189	Sequence 189, App
25	471.5	92.8	663	9	US-09-978-423A-189	Sequence 189, App
26	471.5	92.8	663	9	US-10-013-921A-189	Sequence 189, App
27	471.5	92.8	663	9	US-09-978-193A-189	Sequence 189, App
28	471.5	92.8	663	9	US-10-013-929A-189	Sequence 189, App
29	471.5	92.8	663	9	US-10-016-177A-189	Sequence 189, App
30	471.5	92.8	663	9	US-09-999-830A-189	Sequence 189, App
31	471.5	92.8	663	9	US-09-978-757A-189	Sequence 189, App
32	471.5	92.8	663	9	US-09-978-187B-189	Sequence 189, App
33	471.5	92.8	663	9	US-09-978-643A-189	Sequence 189, App
34	471.5	92.8	663	9	US-10-166-709A-189	Sequence 189, App
35	467.5	92.0	638	9	US-09-822-846-275	Sequence 275, Appl
36	357	70.3	392	9	US-09-871-161-95	Sequence 95, Appl
37	339.5	66.8	363	10	US-09-801-115-7	Sequence 7, Appl1
38	331	65.2	204	10	US-09-801-115-5	Sequence 5, Appl1
39	318.5	62.7	495	9	US-09-978-295A-191	Sequence 191, App
40	318.5	62.7	495	9	US-09-978-697-191	Sequence 191, App
41	318.5	62.7	495	9	US-09-978-192A-191	Sequence 191, App
42	318.5	62.7	495	9	US-09-999-832A-191	Sequence 191, App
43	318.5	62.7	495	9	US-09-978-189-191	Sequence 191, App
44	318.5	62.7	495	9	US-09-978-608A-191	Sequence 191, App
45	318.5	62.7	495	9	US-09-978-191A-191	Sequence 191, App

## ALIGNMENTS

RESULT 1  
US-09-918-995-6534  
; Sequence 6534, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918, 995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235, 076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 6534  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-6534

Alignment Scores:  
Pred. No.: 1.07e-63  
Score: 508.00  
Percent Similarity: 100.00%  
Best local Similarity: 100.00%  
Query Match: 9  
DB: Gaps: 0



Pred. No.:	1,52e-63	Length:	534
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-801-115-1 (1-534)

QY	1	MetaspasnaValGlnProlysIlleLysHisArgProPhecysPheSerVallySGlyHis	20
DB	152	ATGGATTAACGTGACAGCCGAAATAAACAACGCCCTTCGTTCAGTGTGAAGGCCAC	211
QY	21	VallysmetleuArgLeuAspIleIleAsnSerLeuValThrValPheMetleuIle	40
DB	212	GTGAAGATGTCGGCGCTGCATATTATCACTGCTACCAACAGATATCATGCTCACC	271
QY	41	ValserValleuAlaIleuIleProGluThrThrThleuThyValGlyGlyValAlphe	60
DB	272	GTACTCGTGTGGCGACGATACAGAAACCAACAATGCACTTGTTGGAGGGGTGTTT	331
QY	61	AlaIeuValThrAlaValAlcysCysLeuAlaAspGlyAlaIleuIleTyArgLysLeu	80
DB	332	GCACTTGTGACAGAGATGCTGCTCTGGCCGACGGGCCCTTATTACCGAAGCTTCG	391
QY	81	PheAsnProSerGlyProTyrgInLysLysProValHisGluLysGluValIleu	99
DB	392	TTCATCCCAAGCGGTCCCTACCAAGAAAGGCTGTGATGAAAAAAGAAAGTTTG	448

RESULT 6

US-10-106-698-1927

; Sequence 1927, Application US/10106698

; Publication No. US20030109690A1

GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept

; FILE REFERENCE: PA00591

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: PatentIn Ver. 3.0

SEQ ID NO 1927

; LENGTH: 558

; TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (514)..(514)

OTHER INFORMATION: n equals a,t,g, or c

US-10-106-698-1927

Alignment Scores:

Pred. No.:	1,62e-63	Length:	558
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-801-115B-2 (1-99) x US-10-106-698-1927 (1-558)

QY	1	MetaspasnaValGlnProlysIlleLysHisArgProPhecysPheSerVallySGlyHis	20
DB	147	ATGGATTAACGTGACAGCCGAAATAAACAATGCACTTCCTTCAGTGTGAAGGCCAC	206
QY	21	VallysmetleuArgLeuAspIleIleAsnSerLeuValThrValPheMetleuIle	40
DB			

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Db 207 GTGAGATGCTGGCGCTGATATTTATCAACTGATGTAACAAGATATTATTCATGCTCATC 266
Qy 41 ValSerValIleuAlaIleuIleProgluThrThrThrValIglYglYAlaIle 60
Db 267 GTATCTGTGTGGCACTGATACCAAGAACACATTGACAGTGGAGGGGCTTT 326
Qy 61 AlaIleuValThrAlaValIleCysCysIleuAlaAspIglYAlaIleuIleTyrArgIysIleu 80
Db 327 GCACCTGTGACAGCAGTATGCTCTTGGCAGCGGGGCCCTTATTACCGAAGCTTCTG 386
Qy 81 PheAsnProSerGlyProTyrGlnIlyslsProValHisglulYslsIleuValIleu 99
Db 387 TTCATGCCAGCGGCTCTTACCAAGAAAAGCCTGTGCATGAAAAAAGAGTTTGG 443

RESULT 7
US-09-918-995-19489
; Sequence 19489, Application US/09918995
; Publication No. US2003007363A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (1)-(512)
; OTHER INFORMATION: n - A,T,C or G
US-09-918-995-19489

Alignment Scores:
Pred. No.: 1,04e-62 Length: 512
Score: 502.00 Matches: 98
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 1
Query Match: 98.82% Indels: 0
DB: Gaps: 0

US-09-801-115B-2 (1-99) x US-09-918-995-19489 (1-512)
Qy 1 MetaspasValGlnProIlyslsIleYslsHisArgProPhcysPheSerValIlyslsHis 20
Db 142 ATGGATTAACGTGACGCCGAAATAAATCAATCGCCCTTCTGCTTCAAGTGTGAAGGCCAC 201
Qy 21 ValIysMetIleuArgIleuAspIleIleAsnSerIleuValThrThrValPheMetIleuIle 40
Db 202 GTGAAGAGTCTGGCGCTGATATTAATCACTACCTGTAACACAGATTAATCACTCTATC 261
Qy 41 ValSerValIleuAlaIleuIleProgluThrThrThrThrValIglYglYAlaIleuPhe 60
Db 262 GTATCTGTGTGGCACTGATACCAAGAACACCAATTCAGTGTGTGGAGGGGCTTTT 321
Qy 61 AlaIleuValThrAlaValIleCysCysIleuAlaAspIglYAlaIleuIleTyrArgIysIleu 80
Db 322 GCACCTGTGACAGCAGTATGCTCTTGGCAGCGGGGCCCTTATTACCGAAGCTTCTG 381
Qy 81 PheAsnProSerGlyProTyrGlnIlyslsProValHisglulYslsIleuValIleu 99
Db 382 TTCATGCCAGCGGCTCTTACCAAGAAAAGCCTGTGCATGAAAAAAGAGTTTGG 438

RESULT 8
US-09-801-115-3
; Sequence 3, Application US/09801115
; Patent No. US2002000182A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Ma, D.
; APPLICANT: Han, W.
; APPLICANT: Zhang, Y.
; APPLICANT: Song, Q.
; APPLICANT: Di, C.
; APPLICANT: Huang, J.
; APPLICANT: Tang, J.
; APPLICANT: Chen, G.
; TITLE OF INVENTION: CHEMOKINE LIKE FACTOR(CXCLF) WITH CHEMOTACTIC AND HEMATOPOIET
; FILE REFERENCE: 10776-003-999
; CURRENT APPLICATION NUMBER: US/09/801,115
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/CN00/00026
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 99107284.7
; NUMBER OF SEQ ID NOS: 8
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-115-3

Alignment Scores:
Pred. No.: 2.13e-58 Length: 459
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: Gaps: 1

US-09-801-115B-2 (1-99) x US-09-801-115-3 (1-459)
Qy 1 MetaspasValGlnProIlyslsIleYslsHisArgProPhcysPheSerValIlyslsHis 20
Db 1 ATGGATTAACGTGACGCCGAAATAAATCAATCGCCCTTCTGCTTCAAGTGTGAAGGCCAC 60
Qy 21 ValIysMetIleuArgIleuAspIleIleAsnSerIleuValThrThrValPheMetIleuIle 25
Db 61 GTGAAGAGTCTGGCGCTGATATTAATCACTACCTGTAACACAGATTAATCACTCTATC 120
Qy 25 ----- 25
Db 121 GCCCGTAACCATATATTTGTTATCACTGATTTGAAGTACCGGTTATCTTATTTTCATA 180
Qy 26 ----- 26
Db 181 CTTTATATGTAAGTCACTGATGATTCGATTATGAAGTGTATTATTTGGCTTGGCTTGTAT 240
Qy 28 IleIleAsnSerIleuValThrThrValPheMetIleuIleValSerValIleuAlaIleuIle 47
Db 241 ATTATCACTACCTGTAACACAGATTAATCACTGATGATGATGATGATGATGATGATGAT 300
Qy 48 ProgluThrThrThrThrThrValIglYglYAlaIleuPheAlaIleuValThrAlaValIle 67
Db 301 CCAGAAACCAACAATTCAGTGTGTGAAGGGGCTTGGCACTGTGACACAGATATAC 360
Qy 68 CysIleuAlaAspIglYAlaIleuIleTyrArgIysIleuPheAsnProSerGlyProTyr 87
Db 361 TGTCTTGGCGAGCGGGCCCTTATTACCGAAGCTTCTGCTTCAATCCACGAGGCTCTTAC 420
Qy 88 GlnIlyslsProValHisglulYslsIleuValIleuValIleuValIleuValIleuVal 99
Db 421 CAGAAAAGCCTGTGCATGAAAAAAGAGTTTGG 456

RESULT 9
US-09-978-295A-189
; Sequence 189, Application US/09978295A
; Patent No. US2002015606A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

```

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fond, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geiber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/07791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
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US-09-801-115b-2 (1-99) x US-09-978-295A-189 (1-663)

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RESULT 10  
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Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerber, Hanspeter  
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APPLICANT: Kuo, Sophia S.  
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APPLICANT: Pan, James;  
APPLICANT: Paoul, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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## RESULT 11

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## GENERAL INFORMATION:

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 ;; APPLICANT: Botstein, David  
 ;; APPLICANT: Desnoyers, Luc  
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32	PRIOR APPLICATION NUMBER: 60/082700	
33	PRIOR FILING DATE: 1998-04-22	
34	PRIOR APPLICATION NUMBER: 60/082797	
35	PRIOR FILING DATE: 1998-04-22	
36	PRIOR APPLICATION NUMBER: 60/082796	
37	PRIOR FILING DATE: 1998-04-23	
38	PRIOR APPLICATION NUMBER: 60/083366	
39	PRIOR FILING DATE: 1998-04-27	
40	PRIOR APPLICATION NUMBER: 60/083322	
41	PRIOR FILING DATE: 1998-04-28	
42	PRIOR APPLICATION NUMBER: 60/083392	
43	PRIOR FILING DATE: 1998-04-29	
44	PRIOR APPLICATION NUMBER: 60/083455	
45	PRIOR FILING DATE: 1998-04-29	
46	PRIOR APPLICATION NUMBER: 60/083496	
47	PRIOR FILING DATE: 1998-04-29	
48	PRIOR APPLICATION NUMBER: 60/083499	
49	PRIOR FILING DATE: 1998-04-29	
50	PRIOR APPLICATION NUMBER: 60/083545	
51	PRIOR FILING DATE: 1998-04-29	
52	PRIOR APPLICATION NUMBER: 60/083554	
53	PRIOR FILING DATE: 1998-04-29	
54	PRIOR APPLICATION NUMBER: 60/083558	
55	PRIOR FILING DATE: 1998-04-29	
56	PRIOR APPLICATION NUMBER: 60/083559	
57	PRIOR FILING DATE: 1998-04-29	
58	PRIOR APPLICATION NUMBER: 60/083500	
59	PRIOR FILING DATE: 1998-04-29	
60	PRIOR APPLICATION NUMBER: 60/083742	
61	PRIOR FILING DATE: 1998-04-30	
62	PRIOR APPLICATION NUMBER: 60/084366	
63	PRIOR FILING DATE: 1998-05-05	
64	PRIOR APPLICATION NUMBER: 60/084414	
65	PRIOR FILING DATE: 1998-05-06	
66	PRIOR APPLICATION NUMBER: 60/084411	
67	PRIOR FILING DATE: 1998-05-06	
68	PRIOR APPLICATION NUMBER: 60/084637	
69	PRIOR FILING DATE: 1998-05-07	
70	PRIOR APPLICATION NUMBER: 60/084639	
71	PRIOR FILING DATE: 1998-05-07	
72	PRIOR APPLICATION NUMBER: 60/084640	
73	PRIOR FILING DATE: 1998-05-07	

[illegible]

Alignment Scores:	
Pred. No.:	3.66e-58
Score:	471.50
Percent Similarity:	65.13%
Best Local Similarity:	65.13%
Query Match:	92.81%
DB:	9
	9
Length:	665
Matches:	99
Conservative:	0
Mismatches:	0
Indels:	53
Gaps:	1

US-09-801-115B-2 (1-99) x US-09-978-192A-189 (1-663)

OY	I	MetaspasVAlGlnProCysIleLysHSAqPPropHeCsPhSeSerValLeuA1eYHis	20
Dd	131	ATGGATAACCTGCAGCGCAAAATAAACATCCGCCCTTCGTTCAGTGTAAGAACCAC	190
OY	21	VallysMetLeuArg-----	25
Dd	191	GTTGAAGATTGGTGGCGCTGGCACACTGACTHGACATCATAGACCTTTTTATCATGCACA	250
OY	25	-----	25
Dd	251	GCCCCGTGAACCAATATATGTTATACCTGSATTGAAGTACOCGTTATCTTATTTTCATA	310
OY	26	-----LeuAsp	27
Dd	311	CTTTTATATGTAAGTATGATGATGATTAATGAAGTGATTTATTTTGCGCTTTGCTGAT	370
OY	28	IlelleasnSerLeuValThrThraAlpheKetleullelvalSerValLeuAlaleuille	47
Dd	371	ATTATCAACACACTGGTGTAAACAACAGATTCAACGTCAATCATGTATCTGTGTGGCACTGATA	430
OY	48	ProglutThrThrLeuthrValGlyGlyGlyAlaPhealaleuValThrAlalaCys	67
Dd	431	CCAGAAAACCAAACATTGACAGTGGTGGAGGGGTGGCTTGCACCTGTGACAGCAGTATGC	490
OY	68	CysleualaaSpolyalaleuilelyTraDgylsleuleuPheaSnProserGlyProtyr	87
Dd	491	TGCTTTCGCCACGGGGCCCTTATTAAACGGGAAGCTTCGTGTCATATCCAACGGGGTCCTTAC	550
OY	88	GlnLysLyseProValHisglulyslysGiuaValleu	99
Dd	551	CAGAAAAAGCCTGTGCATGAAAAAAAAGAAGTTTGG	586

US-09-999-832A-189  
Sequence 189, Application US/0999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fonf, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Iyar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
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PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689

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PRIOR APPLICATION NUMBER: 60/079663  
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PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
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PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/084366  
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PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
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PRIOR APPLICATION NUMBER: 60/084598  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 3,66e-58 Length: 663  
Score: 471.50 Matches: 99  
Percent Similarity: 65.138 Conservative: 0  
Best Local Similarity: 65.138 Mismatches: 53  
Query Match: 92.818 Indels: 53  
DB: 9 Gaps: 1

US-09-801-115b-2 (1-99) x US-09-999-832A-189 (1-663)

QY 1 MetaspasynValGlnProlystIlelySHlsatgProPhcCysPheSerVallysglyHis 20  
DB 131 ATGATACGTCGACGCGAATAAACAATCCGCCCTTCGCTTCACTGTAAGGCCAC 190  
QY 21 VallyserMetleuarg----- 25  
DB 191 GTGAAGATGCTGCGGCTGCGCACTAAGTGTGACATCTATGACCTTTTATCATCGACAA 250

QY 25 ----- 25  
DB 251 GCCCCTGAACCATATATGTTATCATGACGATTTGAAGTCACCGTATATTTTCANA 310  
QY 26 -----Leuasp 27  
DB 311 CTTTATATGATGACTACAGCTTGATGCATTAATGAGTGTATATTTGGCCTTGCTGAT 370  
QY 28 IlelleanserleuValIthrValPheMetleuIleValserValleuAlaValle 47  
DB 371 ATTATCAACTACACGTAACACAGTATGCTATGCTATCTGTTGCGACGTGATA 430  
QY 48 ProGluThrThrThrleuThrValIglyIglyValPheAlaValIthralaValcys 67  
DB 431 CCAGAACCAACACATGACAGTGTGTGAGAGGCTGTTGCACCTGTGACAGCATATGC 490  
QY 68 CysleuAlaaspGlyAlaValleuIleTyArglyLeuLeuPheAsnProSerGlyProTy 87  
DB 491 TGCTTCGCCGACGGGGGCTTATTTACCGAAGCTTCTGTCAATCCACAGGCTTAC 550  
QY 88 GlnlyslsProValIHisGluLygluValleu 99  
DB 551 CAGAAAAAGCCTGTGCATGAAAAAGAGTTTG 586

RESULT 13  
US-09-978-189-189  
Sequence 189, Application US/09978189  
Publication No. US20030004102A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowskl, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavar, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450

**us-09-801-115b-2.rnpb**

1	PRIOR FILING DATE: 1998-03-10
2	PRIOR APPLICATION NUMBER: 60/07763
3	PRIOR FILING DATE: 1998-03-11
4	PRIOR APPLICATION NUMBER: 60/07764
5	PRIOR FILING DATE: 1998-03-11
6	PRIOR APPLICATION NUMBER: 60/07764
7	PRIOR FILING DATE: 1998-03-11
8	PRIOR APPLICATION NUMBER: 60/07779
9	PRIOR FILING DATE: 1998-03-12
10	PRIOR APPLICATION NUMBER: 60/07800
11	PRIOR FILING DATE: 1998-03-13
12	PRIOR APPLICATION NUMBER: 60/07888
13	PRIOR FILING DATE: 1998-03-20
14	PRIOR APPLICATION NUMBER: 60/07893
15	PRIOR FILING DATE: 1998-03-20
16	PRIOR APPLICATION NUMBER: 60/07929
17	PRIOR FILING DATE: 1998-03-25
18	PRIOR APPLICATION NUMBER: 60/07965
19	PRIOR FILING DATE: 1998-03-26
20	PRIOR APPLICATION NUMBER: 60/07966
21	PRIOR FILING DATE: 1998-03-27
22	PRIOR APPLICATION NUMBER: 60/07968
23	PRIOR FILING DATE: 1998-03-27
24	PRIOR APPLICATION NUMBER: 60/07966
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26	PRIOR APPLICATION NUMBER: 60/07972
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28	PRIOR APPLICATION NUMBER: 60/07978
29	PRIOR FILING DATE: 1998-03-27
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31	PRIOR FILING DATE: 1998-03-30
32	PRIOR APPLICATION NUMBER: 60/07922
33	PRIOR FILING DATE: 1998-03-30
34	PRIOR APPLICATION NUMBER: 60/08010
35	PRIOR FILING DATE: 1998-03-31
36	PRIOR APPLICATION NUMBER: 60/08032
37	PRIOR FILING DATE: 1998-04-01
38	PRIOR APPLICATION NUMBER: 60/08032
39	PRIOR FILING DATE: 1998-04-01
40	PRIOR APPLICATION NUMBER: 60/08032
41	PRIOR FILING DATE: 1998-04-01
42	PRIOR APPLICATION NUMBER: 60/08033
43	PRIOR FILING DATE: 1998-04-01
44	PRIOR APPLICATION NUMBER: 60/08034
45	PRIOR FILING DATE: 1998-04-08
46	PRIOR APPLICATION NUMBER: 60/08104
47	PRIOR FILING DATE: 1998-04-08
48	PRIOR APPLICATION NUMBER: 60/08107
49	PRIOR FILING DATE: 1998-04-08
50	PRIOR APPLICATION NUMBER: 60/08119
51	PRIOR FILING DATE: 1998-04-15
52	PRIOR APPLICATION NUMBER: 60/08181
53	PRIOR FILING DATE: 1998-04-15
54	PRIOR APPLICATION NUMBER: 60/08192
55	PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER:	60/081833
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082566
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082565
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082804
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082700
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
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PRIOR FILING DATE:	1998-04-23
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PRIOR APPLICATION NUMBER:	60/083495
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PRIOR FILING DATE:	1998-04-29
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PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085689
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579

; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	3,66e-58	Length:	663
Score:	471.50	Matches:	99
Percent Similarity:	65.13%	Conservative:	0
Best Local Similarity:	65.13%	Mismatches:	0
Query Match:	92.81%	Indels:	53
		Gaps:	1

US-09-801-115b-2 (1-99) x US-09-978-189-189 (1-663)

QY 1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
 DB 131 ATGATTAACGTGACACCCGAAATATAACATCGCCCTTCTGCTTCACTGTAAGGCCAC 190  
 QY 21 ValLysMetLeuArg----- 25  
 DB 191 GTGAAGATGCTGCGGCTGGCACTACTGTGACATCTAGACCTTTTATCATCGCACAA 250  
 QY 25 ----- 25  
 DB 251 GCCCTGAACCATATATTGTTATCATCTGATTTGAAGTACCGCTTATCTTATTTTCATA 310  
 QY 26 -----Leuasp 27  
 DB 311 CTTTATATATGACTCAGACTGATGATTAATGAAGTGTATTTGGCTTTGCTTGAT 370  
 QY 28 IleIleasnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47  
 DB 371 ATTATCAACTCAGTGTGTAACACAGTATTCATGCTATCTGTGTGGCACTGATA 430  
 QY 48 ProGluThrThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCys 67  
 DB 431 CCAGAAACCCACACACTTGTACACTTGTGTGGAGGGGCTTTGCACTTGTGACACAGTATGC 490  
 QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnProSerGlyProTyr 87  
 DB 491 TGTCTTGGCGAGGGGCCCTTATTTACCGGAAGCTTGTCTCAATCCACAGGGGTCTTAC 550  
 QY 88 GlnLysLysProValHisGluLysGluValLeu 99  
 DB 551 CAGAAAAACCTGTGCATGAAAAAAGAAAGTTTGG 586  
 RESULT 14  
 ; US-09-978-608A-189  
 ; Sequence 189, Application US/09978608A  
 ; Publication No. US20030045462A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Geo, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerlitsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James J.  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2630P1C22  
 ; CURRENT APPLICATION NUMBER: US/09/978,608A  
 ; CURRENT FILING DATE: 2001-10-16  
 ; NUMBER OF SEQ ID NOS: 624  
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 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-978-608A-189

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US-09-801-115b-2 (1-99) x US-09-978-608A-189 (1-663)

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 ; Sequence 189, Application US/09978191A  
 ; Publication No. US20030050239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT FILING DATE: 2001-10-15  
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PRIOR APPLICATION NUMBER: 60/085697

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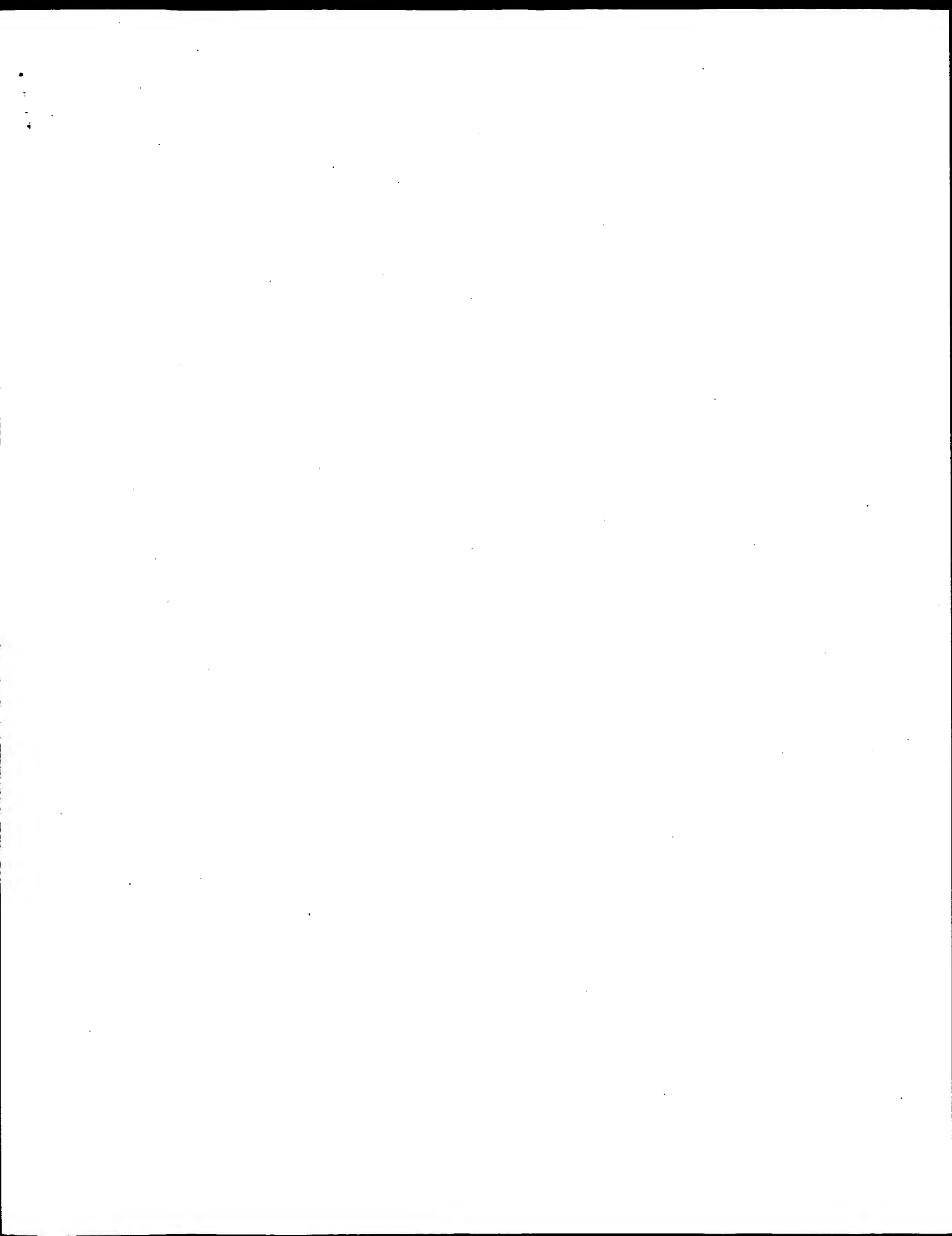
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Score: 471.50 Matches: 99  
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Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115b-2 (1-99) x US-09-978-191A-189 (1-663)

QY 1 MetaspasynValGlnProlysIleLysHisArgProPheCySpheserValLysGlyHis 20  
DB 131 ATGGATACGTGCGCGCGGAAATAAACATCGCCCTTCGCTTCAGTGAAGGCCAC 190  
QY 21 ValLysMetLeuArg----- 25  
DB 191 GTGAAGATGCTGCGCGCGGACGACCTATGACATCTATGACCTTTTATATCATCGCACAA 250  
QY 25 ----- 25  
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DB 371 ATTATCACTCACTGATGATCAACAGTATTCATGCTCATGCTGTGTGGCAGATGATA 430  
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Search completed: June 25, 2003, 14:29:35  
Job time: 138 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 06:26:50 ; Search time 1523 Seconds

(without alignments)  
10204.135 Million cell updates/sec

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Searched: 2054640 segs, 14551402878 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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4	349	65.4	593	9	AF145216	AF145216 Homo sapi
5	338	63.3	688	9	BC004380	BC004380 Homo sapi
6	325.4	60.3	655	9	AF057306	AF057306 Homo sapi
7	321.8	60.3	669	6	AX061665	AX061665 Sequence
8	316.4	59.3	434	9	AF135381	AF135381 Homo sapi
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16	205	38.4	207	6	AX408097	AX408097 Sequence
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DEFINITION Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.  
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VERSION AF096895.2 GI:9989691  
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Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 530)  
Han,W., Lou,Y., Tang,Y., Zhang,Y., Li,Y., Gu,W., Huang,J.,  
Gul,L., Tang,Y., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R.,  
Xia,D., Rull,W., Tang,Y. and Ma,D.

TITLE Molecular cloning and characterization of chemokine-like factor 1 (CKLF1), a novel human cytokine with unique structure and potential chemotactic activity

JOURNAL Biochem. J. 357 (Pt 1), 127-135 (2001)

MEDLINE 21308461

PUBMED 11415443

REFERENCE 2 (bases 1 to 530)

AUTHORS Han, W.L., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and Ma, D.L.

TITLE Direct Submission

JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38 Xue Yuan Rd., Beijing 100083, China

REFERENCE 3 (bases 1 to 530)

AUTHORS Han, W.L.

TITLE Direct Submission

JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China

REMARK Sequence update by submitter

COMMENT On Sep 7, 2000 this sequence version replaced gi:6288733.

FEATURES

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131 CTGGGTCTGACGACGCGATGATACGTGACGCGCGAAGTAAACATCGCCCTT 190

195 TCAAGTGAAGAGCCGACGATGATGCGGCTGATATATCACTCACTGGTAACA 254

191 TCAAGTGAAGAGCCGACGATGATGCGGCTGATATATCACTCACTGGTAACA 250

255 CAGATATTCATGCTATGATGCTGTTGGACGACGACGACGACGACGACGACG 314

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QY 495 TCTGTATTCCTCCAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 534

DB 491 TCTGTATTCCTCCAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 530

RESULT 2

LOCUS AX061624 515 bp DNA linear PAT 24-JAN-2001

DEFINITION Sequence 29 from Patent WO0100806.

ACCESSION AX061624

VERSION AX061624.1 GI:12406709

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 515)

AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

TITLE Complementary dna's encoding proteins with signal peptides

JOURNAL Patent: WO 0100806-A 29 04-JAN-2001; GENSET (FR)

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BASE COUNT 143 a 106 c 135 g 130 t 1 others

ORIGIN

Query Match 92.4%; Score 493.4; DB 6; Length 515; Best Local Similarity 99.4%; Pred. No. 1.1e-110; Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

15 GTGAAGCCGAGCTGGGCGAGAAGTAGAGGAGGGGCTCCGCCGGGTGGCT 74

8 GGGAAAGCCGAGCTGGGCGAGAAGTAGAGGAGGGGCTCCGCCGGGTGGCT 66

75 ATGCGTTCGAGAACCTACCTACGACGACGACGACGACGACGACGACGACG 134

67 ATGCGTTCGAGAACCTACCTACGACGACGACGACGACGACGACGACGACG 126

135 CTGGGTCTGACGACGCGATGATACGTGACGCGCGAAGTAAACATCGCCCTT 194

127 CTGGGTCTGACGACGCGATGATACGTGACGCGCGAAGTAAACATCGCCCTT 186

195 TCAAGTGAAGAGCCGACGATGATGCGGCTGATATATCACTCACTGGTAACA 254

187 TCAAGTGAAGAGCCGACGATGATGCGGCTGATATATCACTCACTGGTAACA 246

255 CAGATATTCATGCTATGATGCTGTTGGACGACGACGACGACGACGACGACG 314

247 CAGATATTCATGCTATGATGCTGTTGGACGACGACGACGACGACGACGACG 306

315 TTGGTGAAGGGGTGTTGACCTGTGACAGCAGATGCTGTTGGCGAGGGGCCCT 374

307 TTGGTGAAGGGGTGTTGACCTGTGACAGCAGATGCTGTTGGCGAGGGGCCCT 366

375 TTTCACGGAAAGCTTCTTCAATCCACGCGGCTCTTACAGAAAAGCCTGTGAT 434

367 TTTCACGGAAAGCTTCTTCAATCCACGCGGCTCTTACAGAAAAGCCTGTGAT 426

QY	435	AAAAAGAGGTTTGTATTTTATATATCTTTTATAGTTGATGACTAAGTATTTAAACATATT	494
Db	427	AAAAAGAGTTTGTATTATTTATTTACITTTTATAGTTTGAATTAAGTATTTAAACATATT	486
QY	495	TCTGTATTCTCCAAAAA	522
Db	487	TCTGTATTCTCCAAAAA	514
RESULT 3			
AF135380		689 bp	linear
AF135380			PRI 07-SEP-2000
LOCUS			
DEFINITION			
AF135380			
VERSION			
KEYWORDS			
ORGANISM			
AF135380.2			
GI:9989692			
REFERENCE			
AF135380			
AUTHORS			
1 (bases 1 to 689)			
Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.			
Direct Submission			
Submitted (17-MAR-1999)			
Immunology, Beijing Medical University, Xue			
Yuan Road, Beijing 100083, China			
2 (bases 1 to 689)			
Han,W.L.			
Direct Submission			
Submitted (07-SEP-2000)			
Immunology, Peking University Health			
Science Center, Xueyuan Road 38, Beijing 100083, China			
Sequence update by submitter			
On Sep 7, 2000 this sequence version replaced gi:6630853.			
REMARK			
COMMENT			
FEATURES			
source			
1..689			
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/cell_line="U937"			
/note="from PHA stimulated cells"			
1..689			
/gene="CKLF2"			
/note="uCK"			
148..606			
/gene="CKLF2"			
/note="uCK-2; alternatively spliced"			
/codon_start=1			
/product="Chemokine-like factor 2"			
/protein_id="AAFI9599.1"			
/db_xref="gi:6630854"			
/translation="MDNVQPKIKRPFCEFSVGVHKMLRLALVTSMTFTFIADAPER			
YIVTGVFVVITFFLLIYLRDRIMKMLFPLDIDINSIVTTFMIVLVLAIDPE			
TTTIVGCGVFAITVAVCCLAGLITRIKLLFNSGPYOKRKVHEKEVYL"			
BASE COUNT			
195 a			
140 c			
161 g			
193 t			
ORIGIN			
Query Match			
Best Local Similarity			
519; Conservative			
65.4%; Score 349.4; DB 9; Length 689;			
76.4%; Pred. No. 2.7e-75;			
0; Mismatches 1; Indels 159; Gaps 1;			
15 GTGAAGCCGAGCTGGGCGACAGAAAGTAGGAGGAGGCGGTCTCCGCGCGGTGGCGGTCT			
74			
11 GGGGAAGCCGAGCTGGGCGACAGAAAGTAGGAGGAGGCGGTCTCCGCGCGGTGGCGGTCT			
70			
75 ATCGCTTGCGAAGAACTACTACGAGGACGAGCTGAGAGAGTGAAGGAAAGTGCTGCTG			
134			
71 ATCGCTTGCGAAGAACTACTACGAGGACGAGCTGAGAGAGTGAAGGAAAGTGCTGCTG			
130			
QY	135	CTGGGCTTCGACAGCGGATGATACGTGACGACCGAAAAATAAAACATCGCCCTCTCTCT	194
Db	131	CTGGGCTTCGACAGCGGATGATACGTGACGACCGAAAAATAAAACATCGCCCTCTCTCT	190
QY	195	TCACGTGTAAAGGCCACGCTGGAAGATGCTGCGGCTG-----	229

Db	191	TCAGTGAAGGCGCAGCTGAAGATGCTGGGCTGGCAGCTAACTGACATCTATGACCT	250
OY	230	-----	229
Db	251	TTTTTATCATCGCACAAGCCCTGAACCAATATGTGTATACACTGGATTTGAAGTCACCG	310
OY	230	-----	229
Db	311	TTATCTATTATTTTCATACCTTTTATATGTACTGAGACTTGATGATTAATGAAGTGGTAT	370
OY	230	-----	229
Db	371	TTTGGCGCTTGCTTGATATATTATCACTCACTGGTAAACAAGATTCATCATCGTAT	430
OY	276	CTGTGTGGGCACTGATACCGAAGAACCAACATTGACAGTTGGTGGAGGGGTGTTGGAC	335
Db	431	CTGTGTGGGCACTGATACCGAAGAACCAACATTGACAGTTGGTGGAGGGGTGTTGGAC	490
OY	336	TTTGGACAGCAGTATGCTGCTTTGGCCAGCGGGGCCCTTATTTACCGGAAGCTCTGTGCA	395
Db	491	TTTGGACAGCAGTATGCTGCTTTGGCCAGCGGGGCCCTTATTTACCGGAAGCTCTGTGCA	550
OY	396	ATCCAGCGGCTCTTACCAGAAAAAGCCTGTGCATGAAAAAAGAAAGTTTGAATTTT	455
Db	551	ATCCAGCGGCTCTTACCAGAAAAAGCCTGTGCATGAAAAAAGAAAGTTTGAATTTT	610
OY	456	ATATTACTTTTATGTTGATGATGATTAACATATTTCTGTATCTTCCAAAAA	515
Db	611	ATATTACTTTTATGTTGATGATGATTAACATATTTCTGTATCTTCCAAAAA	670
OY	516	AAAAAAAAAAAAAAAAAAAA 534	
Db	671	AAAAAAAAAAAAAAAAAAAA 689	
RESULT 4			
LOCUS	AF145216	593 bp	mRNA linear PRI 07-SEP-2000
DEFINITION	Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,		
ACCESSION	AF145216		
VERSION	AF145216.2		
KEYWORDS	GI:9989694		
SOURCE			
ORGANISM	Homo sapiens.		
REFERENCE	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 593) Han,W.L., Gu,W.F., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L. Direct Submission Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China 2 (bases 1 to 593) Han,W.L. Direct Submission Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China Sequence update by submitter On Sep 7, 2000 this sequence version replaced gi:6625671.		
REMARK			
COMMENT			
FEATURES			
source			
gene			
CDS			



373 TGATATATCACTACTGTAACACAGATTCATGTCATGTCATGTTGGACT 432  
Db  
289 GATACACGAACCAACATTCAGTGGTGGAGGGGTTTGCATCTTGACAGCAGT 348  
Qy  
433 GATACACGAACCAACATTCAGTGGTGGAGGGGTTTGCATCTTGACAGCAGT 432  
Db  
349 ATGCTGTCTGCGAGCGGGCCCTTATTTACCGAGCTTCTGTCAATCCAGCGTCC 408  
Qy  
493 ATGCTGTCTGCGAGCGGGCCCTTATTTACCGAGCTTCTGTCAATCCAGCGTCC 552  
Db  
409 TTACCAAAAAAGCCTGTCATGAAAAAAGAGTTTGTATTTATTTACTTTTA 468  
Db  
553 TTACCAAAAAAGCCTGTCATGAAAAAAGAGTTTGTATTTATTTACTTTTA 612  
Qy  
469 GTTGTACTTAAATTAACATTTCTGTATTTCTCAAAAAAATTTTAAAAA 528  
Db  
613 GTTGTACTTAAATTAACATTTCTGTATTTCTCAAAAAAATTTTAAAAA 672  
Qy  
529 AAAAAA 534  
Db  
673 AAAAAA 678

RESULT 6  
AF057306 655 bp mRNA linear PRI 31-DEC-1999  
LOCUS Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.  
DEFINITION AF057306  
ACCESSION AF057306.1 GI:6648618  
VERSION  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 655)  
AUTHORS Zhang, J.S., Nelson, M., Wang, L. and Smith D.I.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-1998) pathology and Lab. Medicine, Mayo Clinic and Foundation, Rochester, MN 55905, USA

FEATURES  
source  
1..655  
/organism="Homo sapiens"  
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/tissue\_type="pancreas"  
/note="adenocarcinoma"  
1..655  
/gene="C32"  
132..590  
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/note="down regulated upon cell differentiation induced by sodium butyrate"  
/product="transmembrane proteolipid"  
/protein\_id="AA2125.1"  
/db\_xref="GI:6648619"  
/translation="MDNVPKIKRHPKPSVKGHYKMLRLATVTSMTFFIIAQP  
YIVTGEVTVILFLLVLRDLRMKMLFPLDIINSLTVFVLMIVSYLALPE  
TTTIVGGGVFALVAVCCADALILRLNPSGPYOKKPVHEKEV"

BASE COUNT 171 a 137 c 153 g 194 t  
ORIGIN

Query Match 60.9%; Score 325.4; DB 9; Length 655;  
Best Local Similarity 75.6%; Pred. No. 2.1e-69;  
Matches 495; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

Qy 21 CCGAGCTGGGCGAGAGTAGGGGAGCGGTGCTCCGCGGTGCGGTGATGCT 80  
Db 1 CCGAGCTGGGCGAGAGTAGGGGAGCGGTGCTCCGCGGTGCGGTGATGCT 60  
Qy 81 TCGCAGAACTACTCAGCAGCCAGCTGAGAGAGTTGAGGAAAGTGTCTGGCT 140  
Db 61 TCGCAGAACTACTCAGCAGCCAGCTGAGAGAGTTGAGGAAAGTGTCTGGCT 120

Qy 141 CTGCAGACGCGATGATTAACGTGACCGCAAAATTAACATGCCCTTCCTCAGTG 200  
Db 121 CTGCAGACGCGATGATTAACGTGACCGCAAAATTAACATGCCCTTCCTCAGTG 180  
Qy 201 TGAAGGCCACGTGAAGATGCTGCGGCTG----- 229  
Db 181 TGAAGGCCACGTGAAGATGCTGCGGCTGCGCACTAAGTGAACATGACCTTTTGA 240  
Qy 230 ----- 229  
Db 241 TCATCGACACAGCCCTGACACATATATTGTTATCATGATTTGAAGTCAACCTTATCT 300  
Qy 230 ----- 229  
Db 301 TATTTTCATCTTTTATATATGATCAGCTGATGATGATTAAGTGTATTTTGGC 360  
Qy 230 -----GATATTAACACTGATGATTAACAGATTCATGCTCATGCTGTGT 281  
Db 361 CTTTGTGATATTAATCACTCATGATTAACAGATTAATTCATGCTCATGCTGTGT 420  
Qy 282 TGGCAGTGAATACCAAGAACCAACATTTACAGTTGCTGAGAGGGTGTGCACTTGA 341  
Db 421 TGGCAGTGAATACCAAGAACCAACATTTACAGTTGCTGAGAGGGTGTGCACTTGA 480  
Qy 342 CAGCAGTATGCTGTGCTGCGAGCGGGCCCTTATTTACGGAAGCTTCTGTCAATCCA 401  
Db 481 CAGCAGTATGCTGTGCTGCGAGCGGGCCCTTATTTACGGAAGCTTCTGTCAATCCA 540  
Qy 402 GCGGCTCTTACCAAGAAAGCCTGTGATGAAAAAAGAGTTTGAATTTATATTA 461  
Db 541 GCGGCTCTTACCAAGAAAGCCTGTGATGAAAAAAGAGTTTGAATTTATATTA 600  
Qy 462 CTTTGTGATGATTAATTAACATTTTCTGTTCTTCCAAAAA 516  
Db 601 CTTTGTGATGATTAATTAACATTTTCTGTTCTTAAAAA 655

RESULT 7  
AX061665 669 bp DNA linear PAT 24-JAN-2001  
LOCUS AX061665  
DEFINITION Sequence 70 from Patent WO010806.  
ACCESSION AX061665  
VERSION AX061665.1 GI:12406789  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 669)  
AUTHORS dums mline Edwards J.B., Bouguetelret L. and Jobert S.  
TITLE Complementary dna's encoding proteins with signal peptides  
JOURNAL Patent: WO 010806-A 70 04-JAN-2001;  
GENSET (FR)

FEATURES  
source  
1..669  
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140..598  
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/db\_xref="GI:12406790"  
/translation="MDNVPKIKRHPKPSVKGHYKMLRLATVTSMTFFIIAQP  
YIVTGEVTVILFLLVLRDLRMKMLFPLDIINSLTVFVLMIVSYLALPE  
TTTIVGGGVFALVAVCCADALILRLNPSGPYOKKPVHEKEV"

BASE COUNT 178 a 139 c 158 g 194 t  
ORIGIN

sig\_peptide  
polya\_signal  
polya\_site  
BASE COUNT 178 a 139 c 158 g 194 t

Query Match	Similarity	60.3%	Score 321.8	DB 6	Length 669
Best Local	Similarity	75.6%	Pred. NO. 1.6e-68		
Matches	504	Conservative	0	Mismatches	2
				Indels	161
				Gaps	2
QY	15	GTGAAGCCGCACTGGGCGAAGAGT	AGGGAGGAGGCGGTCTCCGCCGCGGTGGCGGTTCT	74	
Db	5	GGGAAGCCGCACTGGGCGAAGAGT	AGGGAGGAGGCGGTCTCCGCCGCGGTGGCGGTTCT	64	
QY	75	ATCCCTTGCGAAGACCTCTCCAGCAGCAGCTGAGAAAGT	TGAGGGAAAGTGGTGGTCTG	134	
Db	65	ATCGCTTGCGAAGACCTCTCCAGCAGCAGCTGAGAAAGT	TGAGGGAAAGTGGTGGTCTG	122	
QY	135	CTGGGCTGCGACAGCGCGATGATTAACGTGACGCCGAAATTAACATCGCCCTCTCTCT	194		
Db	123	CTGGGCTGCGACAGCGCGATGATTAACGTGACGCCGAAATTAACATCGCCCTCTCTCT	182		
QY	195	TCAGTGTGAAGGCGCCAGCTGAAGATGCTGGGGCTG	-----	229	
Db	183	TCAGTGTGAAGGCGCCAGCTGAAGATGCTGGGGCTG	-----	229	
QY	230	-----	-----	229	
Db	243	TTTTTATCATGCGACAAAGCCCTGACCATATATTGTTATCATCTGAGATTGTAAGTCACCG	302		
QY	230	-----	-----	229	
Db	303	TTATCTTATTTTTCATCTTATATATGACTCAGACTGATCGATTAATGAAGTGGTTAT	362		
QY	230	-----	-----	229	
Db	363	TTTGGCCCTTCTGATATTTATCATCTCAGCTGTAACACAGTATTCATGCTCATCGTAT	422		
QY	276	CTGTGTGGCAGCTGATATACAGAAACCAACATTTAGACAGTTGGTGGAGGGGTGTTGGCAC	335		
Db	423	CTGTGTGGCAGCTGATATACAGAAACCAACATTTAGACAGTTGGTGGAGGGGTGTTGGCAC	482		
QY	336	TTGTGACAGCGATATGCTGCTTCCGAGCGGGGCCCTTATTTACCGAAGCTTCGTGCA	395		
Db	483	TTGTGACAGCGATATGCTGCTTCCGAGCGGGGCCCTTATTTACCGAAGCTTCGTGCA	542		
QY	396	ATCCAGCGGCTCTTACAGAAAAAGCCGTGATGAAAAAAGAAATTTTGTAAATTTT	455		
Db	543	ATCCAGCGGCTCTTACAGAAAAAGCCGTGATGAAAAAAGAAATTTTGTAAATTTT	602		
QY	456	ATATTAATTTTATTTGATATCTAAGTATTAACATATTTCTGATTTTCTCCAAAAA	515		
Db	603	ATATTAATTTTATTTGATATCTAAGTATTAACATATTTCTGATTTTCTCCAAAAA	662		
QY	516	AAAAAA 522			
Db	663	AAAAAA 669			
RESULT 8					
LOCUS	AF135381	434 bp	mRNA	linear	PRI 07-SEP-2000
DEFINITION					
ACCESSION	AF135381				
KEYWORDS	AF135381.2	GI:9989693			
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
JOURNAL					
REFERENCE					
AUTHORS					
TITLE					
ABSTRACT					
KEYWORDS					
COMMENT					
FEATURES					
ORIGIN					
BASES					
COMMENTS					
REFERENCES					
SEQUENCE					
QUALITY					
DESCRIPTION					
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COMMENTS					
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ORIGIN					
BASES					
COMMENTS					
REFERENCES					
SEQUENCE					
QUALITY					
DESCRIPTION					
FEATURES					
ORIGIN					
BASES					

Journal	Submitted (07-SEP-2000)	Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK	Sequence update by submitter	
COMMENT	On Sep 7, 2000 this sequence version replaced g1:6630855.	
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source	1..434	/organism="Homo sapiens"
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	/note="From PHA stimulated cells"	
gene	1..434	/gene="CXLF3"
	/note="CXLF3"	
	148..351	/note="UCK"
CDS	/gene="CXLF3"	
	/note="UCK-3; alternatively spliced"	
	/codon_start=1	
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	/protein_id="AAF19600.1"	
	/db_xref="GI:6630856"	
	/translation="MDNYOPKIKRHPFCFSVKGHYKMLRLVFLVTAVCCLDALITYI RKLFNPSGPQPKRKYHKEKVL"	
BASE COUNT	127 a	88 c 116 g 103 t
ORIGIN		
Query Match	59.3%; Score 316.4; DB 9; Length 434;	
Best Local Similarity	81.3%; Pred. No. 3.2e-67;	
Matches	423; Conservative 0; Mismatches 1; Indels 96; Gaps 1;	
QY	15 GTGAAGCCGAGCTGGGCGAGAAATGAGGAGGCGGTCTCCGCCGCTGGCGTTGCT	74
DB	11 GGGAAAGCCGAGCTGGGCGAGAAATGAGGAGGCGGTCTCCGCCGCTGGCGTTGCT	70
QY	75 ATCGCTTGCAGAACTCTACTAGCAGCAGCAGCTGAGAGAGTTGAGGAAAGTGTGCTG	134
DB	71 ATCGCTTGCAGAACTCTACTAGCAGCAGCAGCTGAGAGAGTTGAGGAAAGTGTGCTG	130
QY	135 CTGGGCTCGACAGCCGATGATACGTGACAGCCGAAATTAACATGCCCCCTTGTCT	194
DB	131 CTGGGCTCGACAGCCGATGATACGTGACAGCCGAAATTAACATGCCCCCTTGTCT	190
QY	195 TCAGTGTGAAGGCGACGTGAAGATGCTGCGGCTGGATATTATCAACTCACTGGTAACA	254
DB	191 TCAGTGTGAAGGCGACGTGAAGATGCTGCGGCTGGATATTATCAACTCACTGGTAACA	224
QY	255 CAGTATTCATCTCATCTGATCTGTGTGTGGCACTGATATACAGAAACACAACTTGACAG	314
DB	225 -----	224
QY	315 TTGGTGGAGGGGGTGTGCTGCTTGTGAAGAGATAGCTGCTGGCGAGGGGGCCCTTA	374
DB	225 -----GGTGTTCACCTGTGTGACAGCAGTATGCTGTGTCGACAGGGGGCCCTTA	274
QY	375 TTACCGGAACTCTGTGTTCAATCCACAGCGGTCTTACACAGAAAGAGCTGTGCATGAA	434
DB	275 TTACCGGAACTCTGTGTTCAATCCACAGCGGTCTTACACAGAAAGAGCTGTGCATGAA	334
QY	435 AAAAAAGAGTTTGTAAATTTATATATTTACTTTTGTGATACATGATTAATTAACATATT	494
DB	335 AAAAAAGAGTTTGTAAATTTATATATTTACTTTTGTGATACATGATTAATTAACATATT	394
QY	495 TCTGTATTCCTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	534
DB	395 TCTGTATTCCTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	434
RESULT 9		
G30204/c	485 bp	DNA linear STS 05-OCT-1996
LOCUS	human STS SHGC-36487, sequence tagged site.	
ACCESSION	G30204	
VERSION	G30204.1	GI:1593755
KEYWORDS	STS; STS sequence; primer; sequence tagged site.	

SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
JOURNAL 1 (bases 1 to 485)  
COMMENT Myers, R.M.  
Unpublished (1996)

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myerseshgc.stanford.edu

Primer A: ACTCTTTTTCATGACAGG  
Primer B: GCCCTATTACCGAAGCT  
STS size: 77  
PCR Profile:  
Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90565  
-- Washington University/Merck EST sequence.

FEATURES  
source  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/map="16"  
STS  
primer\_bind 69..91  
complement(126..145)  
BASE COUNT 146 a 99 c 99 g 131 t 10 others  
ORIGIN

Query Match 52.1%, Score 278, DB 11; Length 485;  
Best Local Similarity 97.9%; Pred. No. 8.8e-58;  
Matches 281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 226 GCTGATATTACACTGCTGTAACACAGTATGCTGCTATCTGCTGGC 285  
DB 287 GCTTGAATTATACACTGCTGTAACACAGTATGCTGCTATCTGCTGGC 228  
QY 286 ACTGATACCAAGAACCAACATTTGACAGTTGTTGAGGGGTTTCCACTTGTGACAGC 345  
DB 227 ACTGATACCAAGAACCAACATTTGACAGTTGTTGAGGGGTTTCCACTTGTGACAGC 168  
QY 346 AGTATGCTGCTTCCGACGGGCGCTTATTACCGAAGCTTGTGTTCAATCCACGG 405  
DB 167 AGTATGCTGCTTCCGACGGGCGCTTATTACCGAAGCTTGTGTTCAATCCACGG 108  
QY 406 TCCATACCAAGAACCGCTGTCATGAAAAAAGATTGTTGAATTTATATTACTTT 465  
DB 107 TCCATACCAAGAACCGCTGTCATGAAAAAAGATTGTTGAATTTATATTACTTT 48

QY 466 TTAGTTGACTACTAATTAACATATTCTGATCTTCCAAAA 512  
DB 47 TTAGTTGACTACTAATTAACATATTCTGATCTTATATAAA 1

RESULT 10  
AC010289/c  
LOCUS 97083 bp DNA linear pri 06-SEP-2001  
DEFINITION Homo sapiens chromosome 16 clone CTA-989P12, complete sequence.  
AC010289  
VERSION AC010289.9 GI:15451657  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS 1 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission  
REFERENCE 2 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
REFERENCE 3 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (24-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
REFERENCE 4 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (09-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
REFERENCE 5 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
REFERENCE 6 (bases 1 to 97083)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT On Sep 6, 2001 this sequence version replaced gi:15147148.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.8% of Sequence;  
Estimated Total Number of Errors is 0.2.  
STS Content:  
WI-11439 G23701  
WI-15863 G24307  
WI-11780 G23805  
NOTE: A bacterial transposon was excised from this clone at position 96045.

FEATURES  
source  
Location/Qualifiers  
1..97083  
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/db\_xref="taxon:9606"  
/chromosome="16"  
/clone="CTA-989P12"  
BASE COUNT 22777 a 23172 c 24521 g 26613 t  
ORIGIN

Query Match 40.1%; Score 214.4; DB 9; Length 97083;  
Best Local Similarity 99.5%; Pred. No. 8.5e-42;  
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 GTAAAGCCGAGCTGGCGGAGAGTAGGAGGGGCTGCTCGCGCGGCTGCGGCTGCT 74  
I



Db 6753 GGGAGCCGAGCTGGCGGAGAGTAGGGAGGGCGGTCTCCGCCGCGGTGCTGCT 6694  
 QY 75 ATCGCTTCGACAGACCTACTCAGCGCCAGCTGAGAGAGTTGAGGGAGAGTGGTGTG 134  
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 Db 6633 CTGGGCTCTCAGACGGGATGATTAACGTGACAGCCGAAATAAAGATGCCCCCTTCTGCT 6574  
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 LOCUS Homo sapiens clone RP11-13P4, WORKING DRAFT SEQUENCE, 18 unordered  
 DEFINITION pieces.  
 AC018589  
 VERSION AC018589.3 GI:7341919  
 ACCESSION HTG: HTGS\_PHASE1, HTGS\_DRAFT.  
 KEYWORDS Homo sapiens.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Euthera; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 151620)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens, clone RP11-13P4  
 Unpublished  
 2 (bases 1 to 151620)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,  
 Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,  
 Choepel,X., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,  
 DeRellano,K., Dewar,K., Domino,M., Doyle,M., Fensholt,J.,  
 Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,  
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 Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,  
 Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A.  
 and Zody,M.  
 Direct Submission  
 Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 30, 2000 this sequence version replaced gi:6692322.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Genome Center  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L3379  
 Center clone name: L3\_P4  
 Summary Statistics  
 Sequencing vector: M13: M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 141737 bases at least Q40  
 Consensus quality: 145736 bases at least Q30  
 Consensus quality: 147339 bases at least Q20  
 Insert size: 182000; agarose-fp  
 Insert size: 14920; sum-of-ctrls

Quality coverage: 4.6 in Q20 bases; agarose-fp  
 Quality coverage: 5.5 in Q20 bases; sum-of-ctrls  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 18 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 1 1331: contig of 1331 bp in length  
 \* 1332 1431: gap of 100 bp  
 \* 1432 2326: contig of 895 bp in length  
 \* 2327 2426: gap of 100 bp  
 \* 2427 4519: contig of 2093 bp in length  
 \* 4520 4619: gap of 100 bp  
 \* 4620 6916: contig of 2297 bp in length  
 \* 6917 7016: gap of 100 bp  
 \* 7017 10850: contig of 3834 bp in length  
 \* 10851 10950: gap of 100 bp  
 \* 10951 15157: contig of 4207 bp in length  
 \* 15158 15257: gap of 100 bp  
 \* 15258 17752: contig of 2495 bp in length  
 \* 17753 17852: gap of 100 bp  
 \* 17853 22482: contig of 4630 bp in length  
 \* 22483 22583: gap of 100 bp  
 \* 22583 25540: contig of 3958 bp in length  
 \* 25541 26640: gap of 100 bp  
 \* 26641 30917: contig of 4277 bp in length  
 \* 30918 31017: gap of 100 bp  
 \* 31018 36401: contig of 5384 bp in length  
 \* 36402 36501: gap of 100 bp  
 \* 36502 42254: contig of 5753 bp in length  
 \* 42255 42354: gap of 100 bp  
 \* 42355 52974: contig of 10620 bp in length  
 \* 52975 53074: gap of 100 bp  
 \* 53075 62475: contig of 9401 bp in length  
 \* 62476 62575: gap of 100 bp  
 \* 62576 72661: contig of 10086 bp in length  
 \* 72662 72761: gap of 100 bp  
 \* 72762 89410: contig of 16649 bp in length  
 \* 89411 89510: gap of 100 bp  
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 \* 113392 113491: gap of 100 bp  
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Estimated total Number of Errors is 0.5.  
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WT-11439 G23701  
WT-15863 G24307  
SHGC-36487 G30204  
SHGC-11618 G14612  
WT-13905 G22316.

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Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 GTGAAGCCGAGCTGGGAGAGTAGGAGGCGGTCCTCCGCGCGGTGCT 74  
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QY 75 ATGCTTCCGAGAACTTACTCAGGCGAGCCAGCTGAGAAAGTTAGGAAAGTGTGCT 134  
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QY 195 TCAGTGTGAAGGCCACGTGAAGATGCTGGCGCTGG 230  
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DB 71355 TCAGTGTGAAGGCCACGTGAAGATGCTGGCGCTGG 71320  
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RESULT 12  
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LOCUS  
DEFINITION Homo sapiens chromosome 16 clone RP11-403P17, complete sequence.  
ACCESSION AC010542  
VERSION AC010542.7 GI:15042796  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 188460)  
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 188460)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 188460)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Direct Submission  
JOURNAL Submitted (31-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On Jul 31, 2001 this sequence version replaced gi:13786333.  
Draft sequence produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing completed at Stanford Human Genome Center  
www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.5% of Sequence;  
Estimated total Number of Errors is 0.5.  
STS Content:  
WT-11780 G23805  
WT-11439 G23701  
WT-15863 G24307  
SHGC-36487 G30204  
SHGC-11618 G14612  
WT-13905 G22316.

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Location/Qualifiers  
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Best Local Similarity 99.5%; Pred. No. 9.5e-42;  
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 135 CTGGGCTGTCGAGAGCGGATGATTAACGTGCGAGCGGAAATTAACATGCGCCCTTGTCT 194  
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DB 74683 CTGGGCTGTCGAGAGCGGATGATTAACGTGCGAGCGGAAATTAACATGCGCCCTTGTCT 74742  
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QY 195 TCAGTGTGAAGGCCACGTGAAGATGCTGGCGCTGG 230  
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DB 74743 TCAGTGTGAAGGCCACGTGAAGATGCTGGCGCTGG 74778  
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RESULT 13  
AX330610/c 207 bp DNA linear PAT 09-JAN-2002  
LOCUS  
DEFINITION Sequence 1119 from Patent WO0194629.  
ACCESSION AX330610  
VERSION AX330610.1 GI:18103588  
KEYWORDS  
SOURCE human.  
ORGANISM human.  
REFERENCE  
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1  
JOURNAL  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
Patent: WO 0194629-A 1119 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
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Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 207 CAACATTGACAGTGGTGGAGGCGGTGTTGACATTGACAGCAGATGCTGCTGCCG 148  
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QY 363 ACGGGGCCCTTATTATACCGAAGCTTCTGTTCAATCCACAGCGGTCTTACAGAAAAAGC 422  
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Db      147  ACGGGGCCCTTATTACCGAAGCTCTGTCATCCCGCGCTTACCGAAGAAAGC 88
QY      423  CTGTGCATGAAAAAAGAGTTGTGTAATTTATTAATTTAGTTGATTAAGT 482
Db      87   CTGTGCATGAAAAAAGAGTTGTGTAATTTATTAATTTAGTTGATTAAGT 28
QY      483  ATTAACATATTTCTGTATCTTCCA 508
Db      27  ATTAACATATTTCTGTATCTTCCA 2

RESULT 14
AX330787/c 207 bp  DNA  linear  PAT 09-JAN-2002
LOCUS      AX330787
DEFINITION Sequence 1296 from Patent WO0194629.
ACCESSION  AX330787
VERSION     AX330787.1 GI:18103765
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
  AUTHORS   Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
  TITLE     Cancer gene determination and therapeutic screening using signature
  JOURNAL   Patent: WO 0194629-A 1296 13-DEC-2001;
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Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      363  ACGGGGCCCTTATTACCGAAGCTTCTGTCATCCCGAGGCTCTTACCGAAGAAAGC 422
Db      147  ACGGGGCCCTTATTACCGAAGCTTCTGTCATCCCGAGGCTCTTACCGAAGAAAGC 88
QY      423  CTGTGCATGAAAAAAGAGTTGTGTAATTTATTAATTTAGTTGATTAAGT 482
Db      87   CTGTGCATGAAAAAAGAGTTGTGTAATTTATTAATTTAGTTGATTAAGT 28
QY      483  ATTAACATATTTCTGTATCTTCCA 508
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RESULT 15
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LOCUS      AX331008
DEFINITION Sequence 1517 from Patent WO0194629.
ACCESSION  AX331008
VERSION     AX331008.1 GI:18121642
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
  AUTHORS   Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
  TITLE     Cancer gene determination and therapeutic screening using signature

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JOURNAL    Patent: WO 0194629-A 1517 13-DEC-2001;
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Query Match 38.4%; Score 205; DB 6; Length 207;
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Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      303  CAACATTGACAGTTGGTGGAGGGGTGTTGACATGTCACAGCAGTATGCTGTGCGG 362
Db      207  CAACATTGACAGTTGGTGGAGGGGTGTTGACATGTCACAGCAGTATGCTGTGCGG 148
QY      363  ACGGGGCCCTTATTACCGAAGCTTCTGTCATCCCGAGGCTCTTACCGAAGAAAGC 422
Db      147  ACGGGGCCCTTATTACCGAAGCTTCTGTCATCCCGAGGCTCTTACCGAAGAAAGC 88
QY      423  CTGTGCATGAAAAAAGAGTTGTGTAATTTATTAATTTAGTTGATTAAGT 482
Db      87   CTGTGCATGAAAAAAGAGTTGTGTAATTTATTAATTTAGTTGATTAAGT 28
QY      483  ATTAACATATTTCTGTATCTTCCA 508
Db      27  ATTAACATATTTCTGTATCTTCCA 2

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Search completed: June 25, 2003, 11:30:38  
 Job time : 1529 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 05:32:44 ; Search time 217 Seconds

(without alignments)  
5541.784 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534  
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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	534	100.0	534	21	AAA38006
2	507	94.9	655	22	AAA4932
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4	498.2	93.3	538	22	AAH8515
5	497.2	93.1	558	22	AAH8548
6	493.4	92.4	515	21	AAH3435
7	493.4	92.4	515	22	AAH8730
8	486.6	91.1	504	19	AAH5959
9	478.6	89.6	506	19	AAH59746

10	466.8	87.4	500	20	AAH97826	Human secreted pro
11	465.4	87.2	467	21	AAH15929	Human protein clon
12	425	79.6	439	24	AAH36006	CDNA sequence #397
13	411.4	77.0	413	20	AAH97873	Human secreted pro
14	405.4	75.9	415	21	AAH00147	Human secreted pro
15	335	62.7	663	21	AAH34051	Human PRO772 nucle
16	335	62.7	663	21	AAH78498	Human PRO772 nucle
17	335	62.7	663	21	AAH58238	Human PRO772 nucle
18	327.2	61.3	908	22	AAH44933	CDNA encoding nove
19	321.8	60.3	669	22	AAH87771	Human secreted pro
20	321.8	60.3	669	22	AAH64053	CDNA encoding huma
21	309.8	58.0	354	20	AAH41509	Human secreted pro
22	309	57.9	637	21	AAH56747	Human transmembran
23	306.6	57.4	670	24	ABL90366	Human polynucleoti
24	305.8	57.3	638	24	AAH35884	CDNA sequence #275
25	300	56.2	566	22	AAH45120	CDNA encoding nove
26	300	56.2	566	22	AAH45121	CDNA encoding nove
27	295.4	55.3	297	21	AAH15919	Human protein clon
28	285	53.4	544	23	AAH56930	Human prostate exp
29	272	50.9	392	21	AAH16090	Human colon cancer
30	224.4	42.0	459	21	AAH38007	CDNA encoding huma
31	214.4	40.1	5021	22	AAH82407	Human immune/haema
32	214.4	40.1	13744	22	AAH68361	Human immune/haema
33	214.4	40.1	13744	22	AAH82406	Human immune/haema
34	214	40.1	269	21	AAH06850	Human secreted pro
35	210.2	39.4	321	20	AAH97651	Extended human sec
36	205	38.4	207	24	AAH94246	Gene #744 used to
37	205	38.4	207	24	ABL62782	Breast cancer rela
38	205	38.4	207	24	ABL62959	Breast cancer rela
39	205	38.4	207	24	ABL63180	Breast cancer rela
40	201.4	37.7	326	24	AAH057138	Human colon cancer
41	185.2	34.7	495	20	AAH34052	Human EST DNA43509
42	185.2	34.7	495	21	AAH78499	Human EST DNA43509
43	185.2	34.7	495	22	AAH93358	CDNA encoding SRT
44	184.8	34.6	2953	22	AAH68359	Human immune/haema
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#### ALIGNMENTS

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AC AAA38006;
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XX 22-AUG-2000 (first entry)
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XX
XX UCK-1 nucleotide sequence.
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XX
XX
XX UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
KW radiotherapy; chemotherapy; human; ss.
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XX Homo sapiens.
OS
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PN
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XX 14-MAY-1999; 99CN-0107284.
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XX 14-MAY-1999; 99CN-0107284.
PR
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XX 14-MAY-1999; 99CN-0107284.
PA
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XX (UYBE-) UNIV BEIJING MEDICAL.
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XX Ma D, Han W, Zhang Y;
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XX WPI; 2000-388170/34.
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XX P-PSDB; AAH98142.
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XX Chemotactic factor useful for treatment and diagnosis of immunocyte
PT disorders - has immunocyte chemotactic stimulating factor
```



|||||  
Db 1 AGCCGACCTGGGAGAGTAGGGGAGGGGGCTCCGCCGGGTGGCTGCTATCG 60  
Oy 79 CTTCGCGAAGCTTACTAGCAGCAGCCAGCTGAGAGAGTGTAGGGAAAGTCTGCTGG 138  
Db 61 CTTCGCGAAGCTTACTAGCAGCAGCCAGCTGAGAGAGTGTAGGGAAAGTCTGCTGG 120  
Oy 139 GTTCGAGAGCCGATGTAGTACGTGACGCGGAAATTAATCATGCGCCCTTCGCTGAG 198  
Db 121 GTTCGAGAGCCGATGTAGTACGTGACGCGGAAATTAATCATGCGCCCTTCGCTGAG 180  
Oy 199 TGTGAAGGCGACGTGAGATGCTGCGCTGATATTTATCACTAGTGTAAACACAGT 258  
Db 181 TGTGAAGGCGACGTGAGATGCTGCGCTGATATTTATCACTAGTGTAAACACAGT 240  
Oy 259 ATTATGCTCATCTATCTATCTGTGTGACAGTATCCGAAACCAACATTTGACATGG 318  
Db 241 ATTATGCTCATCTATCTATCTGTGTGACAGTATCCGAAACCAACATTTGACATGG 300  
Oy 319 TGGAGGGGTGTTTGCACCTGTGACAGCAGTATGCTGTGCGAGCGGGGCCCTTATTTA 378  
Db 301 TGGAGGGGTGTTTGCACCTGTGACAGCAGTATGCTGTGCGAGCGGGGCCCTTATTTA 360  
Oy 379 CCGGAGGCTTCTGTTCATCCAGCGGCTCTTACACAGAAAAAGCCTGTGATGAAAAA 438  
Db 361 CCGGAGGCTTCTGTTCATCCAGCGGCTCTTACACAGAAAAAGCCTGTGATGAAAAA 420  
Oy 439 AGAAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 498  
Db 421 AGAAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 480  
Oy 499 TATCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 525  
Db 481 TATCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 507

RESULT 3  
AAH98515/c  
ID AAH98515 standard; cDNA: 538 BP.

AC AAH98515;  
DT 12-OCT-2001 (first entry)  
DE Human EST-derived coding sequence SEQ ID NO: 372.  
KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KM diagnostics; forensic test; gene mapping; genetic disorder;  
KM biodiversity; gene therapy; nutrition; ss.  
OS Homo sapiens.  
FN WO200154477-A2.  
XX 02-AUG-2001.  
PD 25-JAN-2001; 2001WO-US02687.  
PF 25-JAN-2001; 2000US-0491404.  
XX 25-JAN-2001; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX (HYSE-) HYSEQ INC.  
PA  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Dimaenac RA, Zhang J, Werhman T;  
XX  
XX MPI: 2001-476164/51.  
DR P-PSDB; AAM23856.  
XX  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use -  
XX  
PS Claim 1; Page 451; 1275pp; English.  
CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention.  
XX  
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Query Match 93.3%; Score 498.2; DB 22; Length 538;  
Best Local Similarity 99.4%; Pred. No. 2,8e-99;  
Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 15 GTGAGCCGAGCTGGGCGAGAGTAGGGAGGCGGCTGCCCGCGGGTGGCTGCT 74  
Db 503 GGGAGCCGAGCTGGGCGAGAGTAGGGAGGCGGCTGCCCGCGGGTGGCTGCT 444  
Oy 75 ATCGCTTCGAGAACTTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAAAGTCTGCTG 134  
Db 443 ATCGCTTCGAGAACTTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAAAGTCTGCTG 384  
Oy 135 CTGGGCTCTGAGCGCGGATGAGTAACTGACGCGGAAATTAATCAATGCGCCCTTCTGCT 194  
Db 383 CTGGGCTCTGAGCGCGGATGAGTAACTGACGCGGAAATTAATCAATGCGCCCTTCTGCT 324  
Oy 195 TCAGTGTGAAGGCGCGAGTGAAGATGCTCGGCTGGATTTATCACTGCTGTATCA 254  
Db 323 TCAGTGTGAAGGCGCGAGTGAAGATGCTCGGCTGGATTTATCACTGCTGTATCA 264  
Oy 255 CAGTATTCATGCTCATCTATCTGTGTGACAGTATCCAGAAACCAACATTTGACAG 314  
Db 263 CAGTATTCATGCTCATCTATCTGTGTGACAGTATCCAGAAACCAACATTTGACAG 204  
Oy 315 TTGGTGGAGGGGTGTTGCACTGTGACAGCAGTATGCTGTGCGAGCGGGGCCCTTA 374  
Db 203 TTGGTGGAGGGGTGTTGCACTGTGACAGCAGTATGCTGTGCGAGCGGGGCCCTTA 144  
Oy 375 TTTCGCGAAGCTTCTGTTCAATCCAGCGGCTCTTACAGAAAAAGCCTGTGATGAAA 434  
Db 143 TTTCGCGAAGCTTCTGTTCAATCCAGCGGCTCTTACAGAAAAAGCCTGTGATGAAA 84  
Oy 435 AAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 494  
Db 83 AAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 24  
Oy 495 TCTGTATTTCTTCCAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTT 517  
Db 23 TCTGTATTTCTTAAAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1

RESULT 4  
AAH98548/c  
ID AAH98548 standard; cDNA: 538 BP.

AC AAH98548;  
DT 12-OCT-2001 (first entry)  
DE Human EST-derived coding sequence SEQ ID NO: 405.  
KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KM diagnostics; forensic test; gene mapping; genetic disorder;  
KM biodiversity; gene therapy; nutrition; ss.  
OS Homo sapiens.  
XX

PX		MO200154477-A2.
PN		
PD		
XX	02 - AUG - 2001.	
XX		
XX	25 - JAN - 2001; 2001WO-US02687.	
PF		
XX	25 - JAN - 2000; 2000US-0491404.	
PR	17 - JUL - 2000; 2000US-0617746.	
PR	03 - AUG - 2000; 2000US-0631451.	
PR	15 - SEP - 2000; 2000US-0663870.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;	
PI	Cao Y, Drmanac RA, Zhang J, Werhman T;	
XX	WPI: 2001-476164/51.	
DR	P-PADB; AAM23889.	
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising	
PT	antibodies and research use -	
PS	Claim 1; Page 467; 1275pp; English.	
XX		
CC	The present invention provides the protein and coding sequences of novel	
CC	proteins from a variety of organisms, including human, dog, cat, horse,	
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea	
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)	
CC	from the organism of interest. They can be used in diagnostics,	
CC	forensics, gene mapping, identification of mutations, to assess	
CC	biodiversity and for nutritional purposes. The present sequence is a cDNA	
XX	sequence.	
SQ	Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;	
Query Match	93.3%; Score 498.2; DB 22; Length 538;	
Best Local Similarity	99.4%; Pred. No. 2.8e-99;	
Matches 500; Conservative	0; Mismatches 3; Indels 0; Gaps 0	
OY	15 GTGAAAGCCGAGCTGGGCGAGAAGTAGGGAGGCGGTCTCCGCCGCGTGGCGTTGCT	74
DB		
	503 GGGAAGCCGACGCTGGGCGAGAGTAGGGAGGCGGTGTCGCCGCCGCGGTGGTCT	444
OY	75 ATGCGCTTGCAAACTCTACTCAGACGACGCACCTAAGAAAGTTGAGGAAAATGCTGCTG	134
DB		
	443 ATGCGCTTGCAAACTCTACTCAGACGACGCACCTAAGAAAGTTGAGGAAAATGCTGCTG	384
OY	135 CTGGGCTCTCAGACGCAGTGAATAAGCTGACGCCGAAATTAACAATCGCCCTTCTGCT	194
DB		
	383 CTGGGCTCTCAGACGCAGTGAATAAGCTGACGCCGAAATTAACAATCGCCCTTCTGCT	324
OY	195 TCAGTGTGAAGAGCCACGTAAGATGCTGGCGCTGATATTATCAACTCATGTAACAA	254
DB		
	323 TCAGTGTGAAGAGCCACGTAAGATGCTGGCGCTGATATTATCAACTCATGTAACAA	264
OY	255 CAGTATTCATGTCATCTATCTGTGGACTGACGTAACAGAAACCAACAATTGACAG	314
DB		
	263 CAGTATTCATGTCATCTATCTGTGGACTGACGTAACAGAAACCAACAATTGACAG	204
OY	315 TTGGTGTGAAGGGGTGTTGCACCTGTGACAGCAGTATGCTCTTGGCGAGGGGCCCTTA	374
DB		
	203 TTGGTGTGAAGGGGTGTTGCACCTGTGACAGCAGTATGCTCTTGGCGAGGGGCCCTTA	144
OY	375 TTAAACCGAAGCTTGTGTCAATCCGACGGCTCTTAAACGAAAAAGCCTGTGCATGAA	434
DB		
	143 TTAAACCGAAGCTTGTGTCAATCCGACGGCTCTTAAACGAAAAAGCCTGTGCATGAA	84
OY	435 AAAAAGAAATTTGTAATTTATATTTATCTTTAGTTGATTAAGTATTAACATATT	494
DB		
	83 AAAAAGAAATTTGTAATTTATATTTATCTTTAGTTGATTAAGTATTAACATATT	24
OY	495 TCTGTAATCTTCCAAAAAAA 517	

[illegible]

OY 136 TGGGTGACAGCGCATGATACGCGCAAGAAATAACATGCGCCCTTCGCTT 195  
 DB 131 TGGGTGACAGCGCATGATACGCGCAAGAAATAACATGCGCCCTTCGCTT 190  
 OY 196 CAGGTGAAAGGCGCAGTGAAGATGCTGCGGTGATATTTATCACTGCTAACAC 255  
 DB 191 CAGGTGAAAGGCGCAGTGAAGATGCTGCGGTGATATTTATCACTGCTAACAC 250  
 OY 256 AGTATTCATGCTCATCTGATCTGTGTGGCAGCATGATCCAGAAACCAACATTGACACT 315  
 DB 251 AGTATTCATGCTCATCTGATCTGTGTGGCAGCATGATCCAGAAACCAACATTGACACT 310  
 OY 316 TGGGAGAGGCGGTGTTTACCTGATGACAGAGTATGCTGCTCCAGCGGCGCTTAT 375  
 DB 311 TGGGAGAGGCGGTGTTTACCTGATGACAGAGTATGCTGCTCCAGCGGCGCTTAT 370  
 OY 376 TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTTTACAGAAAAAGCCTGTGATGAAA 435  
 DB 371 TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTTTACAGAAAAAGCCTGTGATGAAA 430  
 OY 436 AAAAGAGCTTTTGAATTTATTTATTTTACTTTTACTTGTATGATTAATTAATTTT 495  
 DB 431 AAAAGAGCTTTTGAATTTATTTATTTTACTTTTACTTGTATGATTAATTAATTTT 490  
 OY 496 CTGATTTCTTCCAAAAAATTTTAAAAA 522  
 DB 491 CTGATTTCTTCCAAAAAATTTTAAAAA 517

RESULT 6  
 ID AAA87730 standard; cDNA; 515 BP.

AA87730:  
 28-NOV-2000 (first entry)  
 Human secreted protein encoding cDNA SEQ ID #29.

Human; secreted protein; forensic procedure; gene therapy;  
 chromosomal mapping; cancer; autoimmune disease; cardiovascular disorder;  
 cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;  
 brain disorder; skeletal muscle disorder; eye disorder; obesity;  
 mitochondrial cytochrome; diabetes; atherosclerosis; Alzheimer's disease;  
 neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;  
 septic shock; impotence; ss.

OS Homo sapiens.  
 PN WO200037491-A2.  
 PD 29-JUN-2000.  
 PF 20-DEC-1999; 99WO-IB02058.  
 PR 22-DEC-1998; 98US-0113686.  
 PR 25-JUN-1999; 99US-0141032.  
 PA (GENSET) GENSET.

PI Bougueleret L, Dumas J, Duclert A;  
 DR WPI: 2000-442637/38.  
 DR P-PSDB: AAB25768.

XX Polynucleotides and polypeptides encoding proteins with signal  
 PT peptides, useful in diagnostic, forensic, gene therapy and chromosome  
 PT mapping procedures -

PS Claim 1: Page 169-170; 306pp; English.

XX This sequence represents human cDNA encoding a secreted protein. The  
 CC invention relates to sequences AAA87725-A87774 which encode human

CC secreted proteins AAB25763-B25812. The proteins include signal peptides.  
 CC included in the invention are a host cell containing one of the cDNA  
 CC sequences, and a purified antibody capable of binding to one of the  
 CC secreted proteins. Also contained in the invention are methods for  
 CC storing the sequence data on a computer system, and a method for  
 CC identifying features of the cDNA sequences using a computer programme.  
 CC The cDNAs are useful for expressing secreted proteins or fragments to  
 CC obtain antibodies capable of specifically binding to the secreted  
 CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene  
 CC therapy and chromosome mapping procedures and may be used to design  
 CC expression vectors and secretion vectors. The proteins of the invention  
 CC may be used to treat diseases including cancer, autoimmune diseases,  
 CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological  
 CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye  
 CC disorders, obesity, mitochondrial cytochromes, diabetes, atherosclerosis,  
 CC neurodegenerative disorders, graft rejection, Alzheimer's disease,  
 CC dementia, hyperlipidaemia, septic shock and impotence.

CC Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Query Match 92.4%; Score 493.4; DB 21; Length 515;  
 Best Local Similarity 99.4%; Pred. No. 3.1e-98;  
 Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 15 GTGAGCCGAGCTGGGCGAGAGTGAAGGAGGCGGTGCTCCGCGCGGTGGCGTGT 74  
 DB 8 GGGAGCCGAGCTGGGCGAGAGTGAAGGAGGCGGTGCTCCG -CGCGGTGGCGTGTGT 66  
 OY 75 ATGCTTTCGAGAACTTACTCAGGCGAGCGAGTGAAGAGTGAAGGAGGAGTGTGCTG 134  
 DB 67 ATGCTTTCGAGAACTTACTCAGGCGAGCGAGTGAAGAGTGAAGGAGGAGTGTGCTG 126  
 OY 135 CTGGGTCTGAGAGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 194  
 DB 127 CTGGGTCTGAGAGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 186  
 OY 195 TCAAGTGAAGGCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 254  
 DB 187 TCAAGTGAAGGCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 246  
 OY 255 CAGTATTCATGCTCATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314  
 DB 247 CAGTATTCATGCTCATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306  
 OY 315 TTGGTGGAGGGGTTTGGCACTTGTGACAGCAATGCTGCTGCTGCTGCTGCTGCTGCT 374  
 DB 307 TTGGTGGAGGGGTTTGGCACTTGTGACAGCAATGCTGCTGCTGCTGCTGCTGCTGCT 366  
 OY 375 TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTTTACAGAAAAAGCCTGTGATGAAA 434  
 DB 367 TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTTTACAGAAAAAGCCTGTGATGAAA 426  
 OY 435 AAAAGAGCTTTTGAATTTATTTATTTTACTTTTACTTGTATTAATTAATTTT 494  
 DB 427 AAAAGAGCTTTTGAATTTATTTATTTTACTTTTACTTGTATTAATTAATTTT 486  
 OY 495 TCTGTATTTCTTCCAAAAAATTTTAAAAA 522  
 DB 487 TCTGTATTTCTTCCAAAAAATTTTAAAAA 514

RESULT 7  
 AAF64012  
 ID AAF64012 standard; cDNA; 515 BP.

XX AAF64012:  
 05-APR-2001 (first entry)

XX cDNA encoding human secreted protein #13.

XX Secreted protein; prevention; treatment; diagnosis; disease;  
 KW Infection; ds.



ID	AAV59598	standard; DNA; 504 bp.
XX		
AC	AAV59598;	
XX		
DT	06-JAN-1999	(first entry)
XX		
DE	Human secreted protein gene 88 clone HADAV32.	
XX		
KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia	
KW	developmental abnormality; foetal deficiency; blood; allergy; renal; ds;	
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
KW	inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;	
KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus	
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasia.	
XX		
OS	Homo sapiens.	
XX		
PN	W09839448-A2.	
XX		
PD	11-SEP-1998.	
XX		
PF	06-MAR-1998;	98MO-US04493.
XX		
PR	02-OCT-1997;	97US-0061060.
PR	07-MAR-1997;	97US-0038621.
PR	07-MAR-1997;	97US-0040161.
PR	07-MAR-1997;	97US-0040162.

PR	07-MAR-1997	97US-0040333
PR	07-MAR-1997	97US-0040334
PR	07-MAR-1997	97US-0040336
PR	07-MAR-1997	97US-0040626
PR	11-APR-1997	97US-0043311
PR	11-APR-1997	97US-0043312
PR	11-APR-1997	97US-0043313
PR	11-APR-1997	97US-0043314
PR	11-APR-1997	97US-0043358
PR	11-APR-1997	97US-0043369
PR	11-APR-1997	97US-0043376
PR	11-APR-1997	97US-0043578
PR	11-APR-1997	97US-0043580
PR	11-APR-1997	97US-0043669
PR	11-APR-1997	97US-0043670
PR	11-APR-1997	97US-0043671
PR	11-APR-1997	97US-0043672
PR	11-APR-1997	97US-0043674
PR	23-MAY-1997	97US-0047492
PR	23-MAY-1997	97US-0047500
PR	23-MAY-1997	97US-0047501
PR	23-MAY-1997	97US-0047502
PR	23-MAY-1997	97US-0047503
PR	23-MAY-1997	97US-0047581
PR	23-MAY-1997	97US-0047582
PR	23-MAY-1997	97US-0047583
PR	23-MAY-1997	97US-0047584
PR	23-MAY-1997	97US-0047585
PR	23-MAY-1997	97US-0047586
PR	23-MAY-1997	97US-0047587
PR	23-MAY-1997	97US-0047588
PR	23-MAY-1997	97US-0047589
PR	23-MAY-1997	97US-0047590
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PR	23-MAY-1997	97US-0047593
PR	23-MAY-1997	97US-0047594
PR	23-MAY-1997	97US-0047595
PR	23-MAY-1997	97US-0047596
PR	23-MAY-1997	97US-0047597
PR	23-MAY-1997	97US-0047598
PR	23-MAY-1997	97US-0047599
PR	23-MAY-1997	97US-0047600
PR	23-MAY-1997	97US-0047601



[illegible]

Query Match	91.1%;	Score 486.6;	DB 19;	Length 504;
Best Local Similarity	99.0%;	Pred. No. 9,4e-97;		
Matches 500;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
Db	1	CCGAGCTGGGCGAAGATGAGGAGGGCGTCTCCGCGCGGGTGGCGGTGCTATCCGT	80	
OY	21	CCGAGCTGGGCGAAGATGAGGAGGGCGTCTCCGCGCGGGTGGCGGTGCTATCCGT	80	
Db	1	CCGAGCTGGGCGAAGATGAGGAGGGG-C-ACGACCCCGCGGTGGCGTCTATCCGT	59	
OY	81	TGCGACAACTTACTCAGGCGAGCCAGCTGAGAAAGATTGAGGAAAGTGTCTGTGGT	140	
Db	60	TGCGACAACTTACTCAGGCGAGCGACGCTGAGAAAGATTGAGGAAAGTGTCTGTGGT	119	
OY	141	CTGCGACGCCGATGATTAAGTCGACGCCGAAAAATAAACATTCGCCCTTCTGTTCAGTG	200	
Db	120	CTGCGACGCCGATGATTAAGTCGACGCCGAAAAATAAACATTCGCCCTTCTGTTCAGTG	179	
OY	201	TGAAGGCGCAGTGAAGATGCGGCGTGAATATTATCACTACGTCAGTAAACAGTAT	260	
Db	180	TGAAGGCGCAGTGAAGATGCGGCGTGAATATTATCACTACGTCAGTAAACAGTAT	239	
OY	261	TCATGCTCATCGTATCTGTGTGGCATCTGATACAGAAACACAACTTACAGTTGGTG	320	
Db	240	TCATGCTCATCGTATCTGTGTGGCATCTGATACAGAAACACAACTTACAGTTGGTG	299	
OY	321	GAGGGGGTTTGACATCTTGACAGCAGATATCTGTCTGTGCGAGCGGGCCCTATTATAC	380	
Db	300	GAGGGGGTTTGACATCTTGACAGCAGATATCTGTCTGTGCGAGCGGGCCCTATTATAC	359	
OY	381	GGAAGCTTCTGTTCAATCCAGCGGTCTCTTACCAAGAAAAAGCTGTGCATGAAAAAAG	440	
Db	360	GGAAGCTTCTGTTCAATCCAGCGGTCTCTTACCAAGAAAAAGCTGTGCATGAAAAAAG	419	
OY	441	AAAGTTTGTAAATTTATTTACTTTTGTGATTAAGTATTAAACATATTTCGTA	500	
Db	420	AAAGTTTGTAAATTTATTTACTTTTGTGATTAAGTATTAAACATATTTCGTA	479	
OY	501	TTCTCCAAAAAATAAAAAAAAAA 525		
Db	480	TTCTCCAAAAAATAAAAAAAAAA 504		
RESULT 9				
AAV59746				
ID	AAV59746 standard; DNA; 506 BP.			
AC	AAV59746;			
XX	19-JAN-1999 (first entry)			
DE	Human secreted protein gene 88 clone HANAV32.			
XX	Human: secreted protein; fusion protein; gene therapy; protein therapy;			
KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;			
KW	developmental abnormality; foetal deficiency; blood, allergy; renal; ds;			
KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;			
KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;			
KW	cognitive disorder; schizophrenia; prostase; obesity; osteoclast; thymus;			
KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;			
KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.			
XX				

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OS Homo sapiens.
XX
XX MO9839448-A2.
XX
PD 11-SEP-1998.
XX
XX 06-MAR-1998; 98MO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043566.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043677.
PR 23-MAY-1997; 97US-0043679.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 06-JUN-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 13-JUN-1997; 97US-0048974.
PR 08-JUL-1997; 97US-0049610.
PR 16-JUL-1997; 97US-0051926.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.

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PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056665.
PR 22-AUG-1997; 97US-0056682.
PR 22-AUG-1997; 97US-0056684.
PR 22-AUG-1997; 97US-0056687.
PR 22-AUG-1997; 97US-0056688.
PR 22-AUG-1997; 97US-0056689.
PR 22-AUG-1997; 97US-0056690.
PR 22-AUG-1997; 97US-0056691.
PR 22-AUG-1997; 97US-0056692.
PR 22-AUG-1997; 97US-0056693.
PR 22-AUG-1997; 97US-0056694.
PR 22-AUG-1997; 97US-0056698.
PR 22-AUG-1997; 97US-0056808.
PR 22-AUG-1997; 97US-0056809.
PR 22-AUG-1997; 97US-0056910.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.

XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress CA,
XX Feng P, Ferris AM, Fischer CL, Florence KA, Greene JM, Hu JS,
XX Kraw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
XX Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX WPI; 1998-506364/43.
XX P-PSDB; AAW74961.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
XX - useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 472; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 88 from
XX the human cDNA clone HANA9V2 (deposited as clone ATCC 97897 and ATCC
XX 209043) which encodes a secreted human protein. The gene can be used to
XX generate fusion proteins by linking to the gene to a human
XX immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
XX the fused protein as compared to the human protein only.
XX CC The invention relates to 186 novel genes and their fragments (nucleic
XX acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 186
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAV59511 for described uses).
XX
XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;

```

```

Query Match      89.6%; Score 478.6; DB 19; Length 506;
Best Local Similarity 97.4%; Pred. No. 5.2e-95;
Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

```



KM septic shock; sepsis; ischaemia, reperfusion injury; arthritis; tumour;  
 KM nephritis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 PN WO200005367-A2.  
 PD 03-FEB-2000.  
 XX  
 PF 22-JUL-1999; 99MO-JP03929.  
 PR 24-JUL-1998; 98JP-0208820.  
 PR 07-AUG-1998; 98JP-0224105.  
 PR 25-AUG-1998; 98JP-0238116.  
 PR 09-SEP-1998; 98JP-0254736.  
 XX 29-SEP-1998; 98JP-0275505.  
 PA (SAGA ) SAGAMI CHEM RES CENT.  
 PA (PROT-) PROTEGENE INC.  
 PI Kato S, Kimura T;  
 DR WPI: 2000-182694/16.  
 DR P-PSDB: AAY94861.  
 XX  
 PT Novel human proteins having hydrophobic domains useful for treating  
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,  
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -  
 XX  
 PS Claim 4; Page 228; 351pp; English.  
 XX  
 This sequence encodes a human protein of the invention, which has  
 hydrophobic domains. The DNA sequences can be used as a probe or as a  
 genetic marker. The protein can also be used as a marker, and to identify  
 potential genetic disorders. The DNA and protein can also be used as  
 nutritional sources or supplements. The protein exhibits cytokine, cell  
 proliferation, cell differentiation activities and induces production of  
 other cytokines in certain cell populations. The protein also exhibits  
 immune stimulating or immune suppressing activity. It can be used in the  
 treatment of various immune deficiencies and disorders, and to treat  
 infectious diseases caused by viral, bacterial, fungal or other  
 infections. The protein is also used for treating autoimmune disorders  
 such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid  
 arthritis. It is also useful in the treatment of allergic reactions and  
 conditions such as asthma, and in immune suppression after organ  
 transplantation. The protein is useful in regulation of haematopoiesis  
 and consequently in the treatment of myeloid or lymphoid cell  
 deficiencies. It is also used in compositions for tissue growth or  
 regeneration. The protein is also used in the treatment of osteoporosis  
 or osteoarthritis and in the treatment of periodontal disease and other  
 tooth repair processes. The protein is used in the treatment of nervous  
 system disorders such as Alzheimer's disease, Parkinson's disease, and  
 Huntington's disease. They are useful for protection or regeneration and  
 treatment of lung or liver fibrosis, reperfusion injury in various  
 tissues, and conditions resulting from systemic cytokine damage. They are  
 also used for promoting or inhibiting tissue differentiation. They are  
 also used as contraceptives since they exhibit activin or inhibin related  
 activities and as a fertility inducing therapeutic. They are used for  
 treating various coagulation disorders and in treatment and prevention of  
 conditions resulting from coagulation activities e.g. myocardial  
 infarction or stroke. They also acts as receptors, receptor ligands or  
 inhibitors or agonists of receptor/ligand interactions. They are used to  
 treat inflammatory conditions such as septic shock, sepsis, ischemia  
 reperfusion injury, arthritis, and nephritis. They can be used to  
 prevent tumours.  
 XX  
 Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;  
 SO  
 Query Match 87.2%; Score 465.4; DB 21; Length 467;  
 Best Local Similarity 99.8%; Pred. No. 3.8e-92;  
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0  
 39 AGGGAGAGGGCGGTCTCCGCGCGGATGGCGGTTCATGCGCTTCGCGAAGACTTACTCAGG 98

Db	1	AGGGGAGGCGGCTGCTCCGCCGGGCGGTGGCGGTTGCTATGCTTCCGAGAACTACTACAGG	60
Oy	99	CAGCCAGCTGAGAAAGATGTGAGGGAAGTGTGCTGCTGCTGGGTCTGCAGACGGGATGATA	158
Db	61	CAGCCAGCTGAGAAAGATGTGAGGGAAGTGTGCTGCTGCTGGGTCTGCAGACGGGATGATA	120
Oy	159	ACGTGCAGCCGAAATTAACATCATCGCCCTTCCTGCTTCAGTGTGAAGGCCACGTGAAGA	218
Db	121	ACGTGCAGCCGAAATTAACATCATCGCCCTTCCTGCTTCAGTGTGAAGGCCACGTGAAGA	188
Oy	219	TGCTGCGGGCTGCGATATATATCACTCACTGGTAACAACAGTATTCATGCTCATGTCGTG	278
Db	181	TGCTGCGGGCTGCGATATATATCACTCACTGGTAACAACAGTATTCATGCTCATGTCGTG	240
Oy	279	TGTTGGCAGCATATACCAAGAACACAACTATGACAGTTGGTGGAGGGGTGTTTCACCTG	338
Db	241	TGTTGGCAGCATATACCAAGAACACAACTATGACAGTTGGTGGAGGGGTGTTTCACCTG	300
Oy	339	TGACAGCAGTATGCTGCTGTCGCGCAGCGGGGCCCTTATTTAACCGAAGCTTCGTTCATC	398
Db	301	TGACAGCAGTATGCTGCTGTCGCGCAGCGGGGCCCTTATTTAACCGAAGCTTCGTTCATC	360
Oy	399	CCAGCGGCTCCTTACCCAGAAAAGCCCTGTGCATGAGAAAAAGAGTTTGTATTTATA	458
Db	361	CCAGCGGCTCCTTACCCAGAAAAGCCCTGTGCATGAGAAAAAGAGTTTGTATTTATA	420
Oy	459	TTACTTTTATGTTGATTAAGTATTAACATATTTCTGTATCTT	505
Db	421	TTACTTTTATGTTGATTAAGTATTAACATATTTCTGTATCTT	467

RESULT 12

ABK36006	standard; cDNA: 439 BP.
ABK36006	
ABK36006	
08-MAY-2002	(first entry)
cdna sequence #397 encoding, novel human secreted protein.	
Human secreted protein: hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infections disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.	
Homo sapiens.	
W0200177289-A2.	
18-OCT-2001.	
29-MAR-2001; 2001WO-US10232.	
06-APR-2000; 2000US-195605P.	
(GEMT ) GENNETICS INST INC.	
Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;	
Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;	
Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;	
WPI; 2002-179322/23.	
Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders	
Claim 1; Page 296-297; 393pp; English.	

CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
 CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),  
 CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.  
 CC haemophilia), and tumours. The polynucleotide sequences of the  
 CC invention are also useful in gene therapy. ABK35610-ABK36232 represent  
 CC the cDNA sequences of the invention that encode for novel human  
 CC secreted proteins.

XX Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;

Query Match 79.6%; Score 425; DB 24; Length 439;

Best Local Similarity 99.8%; Pred. No. 2.3e-83; Matches 436; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

DB 72 GGTATCGCTGGCAGAACTCTACTGAGCCAGCTGAGAGAGTGAAGGAAAGTGTG 131  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1 GGTATCGCTGGCAGAACTCTACTGAGCCAGCTGAGAGAGTGAAGGAAAGTGTG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 132 CTGCTGGGTCTGCAGACGCGATGATTAACGTCAGCCGAAATAAACATCGCCCTTCT 191  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 61 CTGCTGGGTCTGCAGACGCGATGATTAACGTCAGCCGAAATAAACATCGCCCTTCT 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 132 GCTTACAGTGTGAAGAGCCAGCAGATGCTGGGCTGGATTTTCAACACACGTA 251  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 121 GCTTACAGTGTGAAGAGCCAGCAGATGCTGGGCTGGATTTTCAACACGTA 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 252 CAACAGTATTCATGCTCATGCTGATGCTGGTGGACACTGATACAGAAACCAACATTTGA 311  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 181 CAACAGTATTCATGCTCATGCTGATGCTGGTGGACACTGATACAGAAACCAACATTTGA 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 312 CAGTTGGTGGAGGGGTGTTTGACATGTGACAGCAGATGCTGCTTCCGACGGGGCC 371  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 241 CAGTTGGTGGAGGGGTGTTTGACATGTGACAGCAGATGCTGCTTCCGACGGGGCC 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 372 TTATTTACCGGAGCTCTGTTCAATCCACGGGCTCTTACAGAAAGAGCTGTGATG 431  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 301 TTATTTACCGGAGCTCTGTTCAATCCACGGGCTCTTACAGAAAGAGCTGTGATG 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 432 AAAAAAGAGAGTTTGTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 490  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 361 AAAAAAGAGAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 491 TATTTCTGTATTTCTTCC 507  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 421 TATTTCTGTATTTCTTCC 437  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

# RESULT 13

AAK97873  
 ID AAK97873 standard; cDNA; 413 BP.

XX AAK97873;

DT 23-SEP-1999 (first entry)

XX Human secreted protein encoding cDNA #61.

XX Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;

KM diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

OS Homo sapiens.

XX

PN WO925825-A2.

XX 27-MAY-1999.

PD 13-NOV-1998; 98WC-IB01862.

XX 04-SEP-1998; 98US-0092973.

PR 13-NOV-1997; 97US-0066677.

PR 17-DEC-1997; 97US-0069957.

PR 09-FEB-1998; 98US-0074121.

PR 13-APR-1998; 98US-0081563.

PR 10-AUG-1998; 98US-0096116.

XX (BEST) GENSET.

XX Bougueleret L, Duclert A, Dumas Milne Edwards J;

XX WPI: 1999-347472/29.

DR P-PSDB; AAY36189.

XX Extended cDNAs encoding secreted proteins

PT Claim 1; Page 261; 307pp; English.

XX AAK97813-X97906 represent extended cDNA's which encode novel human

CC secreted proteins (see AAY36129-Y36222) and which have cytosolic,

CC thrombotic and osteopathic activity. The extended cDNAs can be used to

CC express secreted proteins or parts of them or to obtain antibodies

CC capable of binding to the secreted proteins. They may also be used in

CC diagnostic, forensic, gene therapy and chromosome mapping procedures.

CC Uses also include design of expression vectors and secretion vectors.

XX Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;

Query Match 77.0%; Score 411.4; DB 20; Length 413;

Best Local Similarity 99.8%; Pred. No. 2.1e-80; Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 107 TGAGAGAGTTGAGGAGAAAGTGTGCTGCTGGGCTGTGACAGCGCATGATTAACGTGCAG 166  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1 TGAGAGAGTTGAGGAGAAAGTGTGCTGCTGGGCTGTGACAGCGCATGATTAACGTGCAG 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 167 CCGAAATTAATTAACATCGCCCTTCTGCTTCAAGTGTGAAGCCACAGTGAAGTGTGCGG 226  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 61 CCGAAATTAATTAACATCGCCCTTCTGCTTCAAGTGTGAAGCCACAGTGAAGTGTGCGG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 227 CTGATATTTATCACTCACTGCTGTAAACAGTATTCATGCTCATGCTGTGTGCA 286  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 121 CTGATATTTATCACTCACTGCTGTAAACAGTATTCATGCTCATGCTGTGTGCA 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 287 CTGATATTTATCACTCACTGCTGTAAACAGTATTCATGCTCATGCTGTGTGCA 346  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 181 CTGATATTTATCACTCACTGCTGTAAACAGTATTCATGCTCATGCTGTGTGCA 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 347 GTATGCTGTCTTGGCGAGGGGGCTTATTTACCGGAAGCTTCTGTTCAATCCACGGGT 406  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 241 GTATGCTGTCTTGGCGAGGGGGCTTATTTACCGGAAGCTTCTGTTCAATCCACGGGT 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 407 CCTTACCGAAGAAAGCCGTGTCATGTAAGAAAGAAAGTGTGTAATTTATTTACTTTT 466  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 301 CCTTACCGAAGAAAGCCGTGTCATGTAAGAAAGAAAGTGTGTAATTTATTTACTTTT 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 467 TAGTTGATTAAGTATTAACATATTTCTGTAATTTCTTCCAAAAA 519  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 361 TAGTTGATTAAGTATTAACATATTTCTGTAATTTCTTCCAAAAA 413  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

# RESULT 14

AAK00147  
 ID AAK00147 standard; cDNA; 415 BP.

XX AAK00147;

DT 06-OCT-2000 (first entry)

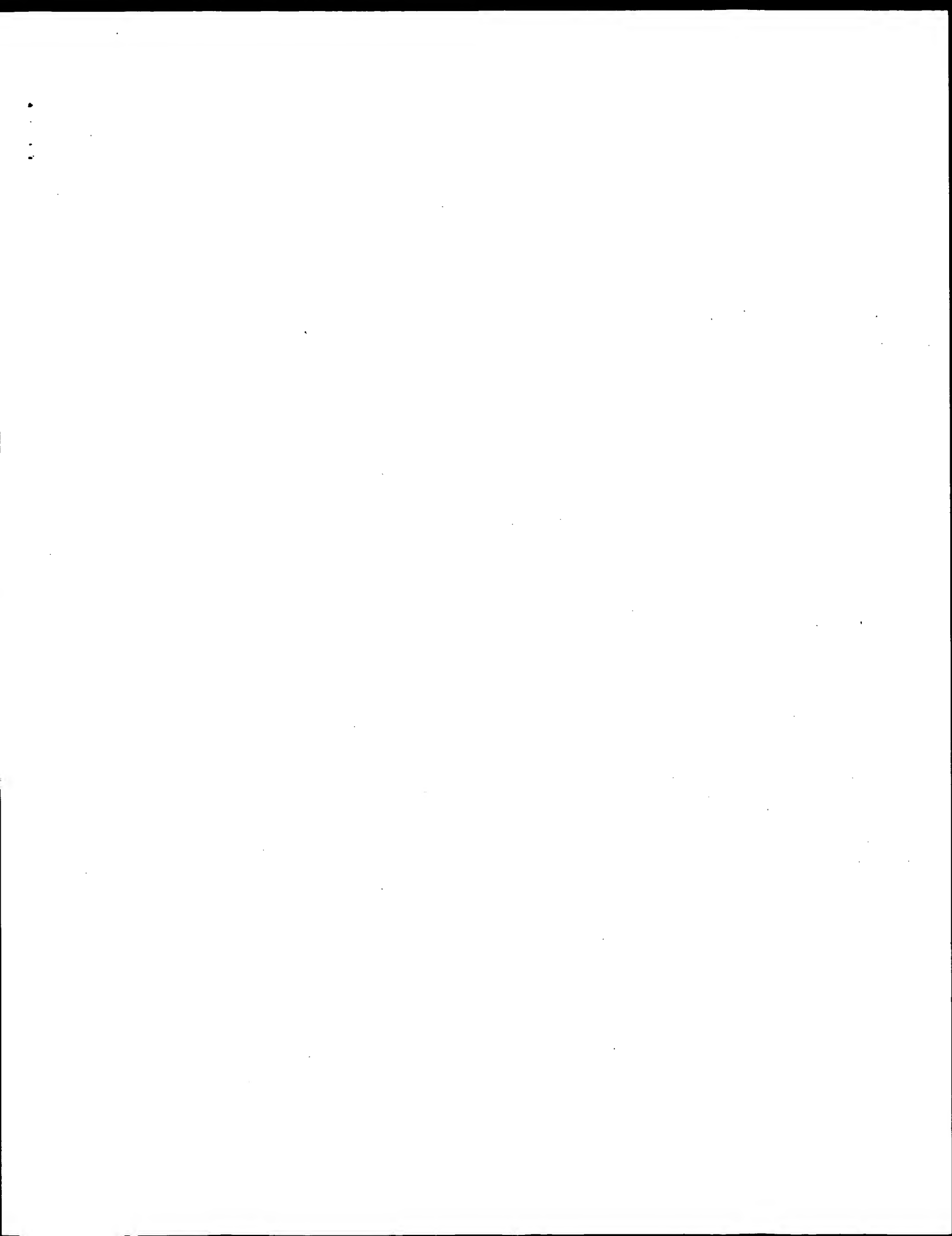
Qy	375	TTTTCCGGAAGCTTCGTTCATCCAGGCGCTTACCGAAGAAAG	421
Db	369	TTTACCGGAAGCTTCGTTCATCCAGGCGCTTACCGAAGAAAG	415
RESULT 15			
AAZ34051			
ID	AAZ34051	standard; cDNA; 663 BP.	
XX	AAZ34051;		
AC			
XX			
DT	07-DEC-1999	(first entry)	
XX			
DE	Human PRO772	nucleotide sequence.	
XX			
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;		
KM	probe; blood coagulation disorder; cancer; cellular adhesion disorder;		
XX	secreted protein; transmembrane protein; ss.		
OS	Homo sapiens.		
XX			
PN	W03946281-A2.		
XX			
PD	16-SEP-1999.		
XX			
PF	08-MAR-1999;	99WO-US05028.	
XX			
PR	10-MAR-1998;	98US-0077450.	
PR	11-MAR-1998;	98US-0077632.	
PR	11-MAR-1998;	98US-0077641.	
PR	11-MAR-1998;	98US-0077649.	
PR	12-MAR-1998;	98US-0077791.	
PR	13-MAR-1998;	98US-0078004.	
PR	17-MAR-1998;	98US-0040220.	
PR	20-MAR-1998;	98US-0078886.	
PR	20-MAR-1998;	98US-0078910.	
PR	20-MAR-1998;	98US-0078939.	
PR	20-MAR-1998;	98US-0079294.	
PR	25-MAR-1998;	98US-0079656.	
PR	26-MAR-1998;	98US-0079663.	
PR	27-MAR-1998;	98US-0079664.	
PR	27-MAR-1998;	98US-0079689.	
PR	27-MAR-1998;	98US-0079728.	
PR	27-MAR-1998;	98US-0079786.	
PR	30-MAR-1998;	98US-0079920.	
PR	30-MAR-1998;	98US-0079923.	
PR	31-MAR-1998;	98US-0080105.	
PR	31-MAR-1998;	98US-0080107.	
PR	31-MAR-1998;	98US-0080165.	
PR	01-APR-1998;	98US-0080327.	
PR	01-APR-1998;	98US-0080328.	
PR	01-APR-1998;	98US-0080333.	
PR	01-APR-1998;	98US-0080334.	
PR	08-APR-1998;	98US-0081049.	
PR	08-APR-1998;	98US-0081070.	
PR	08-APR-1998;	98US-0081071.	
PR	09-APR-1998;	98US-0081195.	
PR	09-APR-1998;	98US-0081203.	
PR	09-APR-1998;	98US-0081229.	
PR	15-APR-1998;	98US-0081817.	
PR	15-APR-1998;	98US-0081838.	
PR	15-APR-1998;	98US-0081952.	
PR	15-APR-1998;	98US-0081955.	
PR	21-APR-1998;	98US-0082568.	
PR	21-APR-1998;	98US-0082569.	
PR	22-APR-1998;	98US-0082700.	
PR	22-APR-1998;	98US-0082704.	
PR	23-APR-1998;	98US-0082804.	
PR	23-APR-1998;	98US-0082767.	
PR	23-APR-1998;	98US-0082796.	

PR	27-APR-1998;	98US-0083336.
PR	28-APR-1998;	98US-0083332.
PR	29-APR-1998;	98US-0083392.
PR	29-APR-1998;	98US-0083495.
PR	29-APR-1998;	98US-0083496.
PR	29-APR-1998;	98US-0083499.
PR	29-APR-1998;	98US-0083500.
PR	29-APR-1998;	98US-0083545.
PR	29-APR-1998;	98US-0083554.
PR	29-APR-1998;	98US-0083558.
PR	29-APR-1998;	98US-0083559.
PR	30-APR-1998;	98US-0083742.
PR	05-MAY-1998;	98US-0084366.
PR	06-MAY-1998;	98US-0084414.
PR	06-MAY-1998;	98US-0084441.
PR	07-MAY-1998;	98US-0084598.
PR	07-MAY-1998;	98US-0084600.
PR	07-MAY-1998;	98US-0084627.
PR	07-MAY-1998;	98US-0084637.
PR	07-MAY-1998;	98US-0084639.
PR	07-MAY-1998;	98US-0084640.
PR	13-MAY-1998;	98US-0085323.
PR	13-MAY-1998;	98US-0085333.
PR	13-MAY-1998;	98US-0085339.
PR	15-MAY-1998;	98US-0085573.
PR	15-MAY-1998;	98US-0085579.
PR	15-MAY-1998;	98US-0085580.
PR	15-MAY-1998;	98US-0085582.
PR	15-MAY-1998;	98US-0085689.
PR	15-MAY-1998;	98US-0085697.
PR	15-MAY-1998;	98US-0085700.
PR	15-MAY-1998;	98US-0085704.
PR	18-MAY-1998;	98US-0086023.
PR	22-MAY-1998;	98US-0086392.
PR	22-MAY-1998;	98US-0086414.
PR	22-MAY-1998;	98US-0086430.
PR	22-MAY-1998;	98US-0086486.
PR	28-MAY-1998;	98US-0087098.
PR	28-MAY-1998;	98US-0087106.
PR	28-MAY-1998;	98US-0087208.
PR	30-JUL-1998;	98US-0094651.
PR	11-SEP-1998;	98US-0100038.
PA	(GETH ) GENENTECH INC.	
PI	Wood WT, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
XX	WPI, 1999-551358/46.	
DR	P-PSDB; AAY41713.	
XX	New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -	
PT		
PT		
XX	Claim 2; Fig 69; 530P; English.	
PS		
XX	The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as	
CC	sources of probes, primers, for chromosome mapping, and for generation	
CC	of antisense sequences. They can also be used to create transgenic	
CC	animals. The proteins can be used to treat a variety of diseases and	
CC	disorders, depending on their function. Diseases that may be treated	
CC	include blood coagulation disorders, cancers and cellular adhesion	
CC	disorders. They may also be used to raise antibodies. AA23891 to	
CC	AA34338, and AAY4185 to AAY1774 represent polynucleotide and	
CC	polypeptide sequence given in the exemplification of the present	
CC	invention.	
XX		
XX	Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;	
XX		
Query Match	62.7%; Score 335; DB 20; Length 663;	
Best Local Similarity	76.0%; Pred. No. 9.8e-64;	

	Matches	504;	Conservative	0;	Mismatches	0;	Indels	159;	Gaps	1
OY	22	CGAGCTGGGCGAGAA	GTG	GGG	GAG	GCG	GCTGCTCCGCGCGGTG	GCTGATATC	GCTT	81
Db	1	CGAGCTGGGCGAGAA	GTG	GGG	GAG	GCG	GCTGCTCCGCGCGGTG	GCTGATATC	GCTT	60
OY	82	CGCAGAACCTTACT	CGAG	CAG	CGT	TGAG	AGAGT	TGAG	GGG	141
Db	61	CGCAGAACCTTACT	CGAG	CAG	CGT	TGAG	AGAGT	TGAG	GGG	120
OY	142	TGCAGACGCGAT	TGAT	TAAC	TGAC	GCCG	CAAAA	TAATAA	ATCGCC	201
Db	121	TGCAGACGCGAT	TGAT	TAAC	TGAC	GCCG	CAAAA	TAATAA	ATCGCC	180
OY	202	GAAAGGCCACGT	GAA	GAT	GTG	CGG	CTG	-----	-----	229
Db	181	GAAAGGCCACGT	GAA	GAT	GTG	CGG	CTG	-----	-----	240
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OY	523	AAA	525							
Db	661	AAA	663							

Search completed: June 25, 2003, 10:42:47  
Job time : 219 secs

Query Match	62.7%;	Score 335;	DB 20;	Length 663;
Best Local Similarity	76.0%;	Pred. No. 9.8e-64;		





GenCore version 5.1.6  
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OW nucleic - nucleic search, using sw model

Run on: June 25, 2003, 10:08:11 ; Search time 65 Seconds  
(without alignments)  
2519.468 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534

Sequence: 1 gtccccaactctgaagtagaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

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6: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	486.6	91.1	504	US-09-149-476-98	Sequence 98, Appl
2	478.6	89.6	506	US-09-149-476-252	Sequence 252, App
3	272	50.9	392	US-09-385-982-95	Sequence 95, Appl
4	50.4	9.4	1582	US-08-545-196B-10	Sequence 10, Appl
5	50.4	9.4	1582	US-08-545-196B-12	Sequence 12, Appl
6	46.8	8.8	770	US-08-865-297-5	Sequence 5, Appl
7	45.8	8.6	3761	US-08-890-865A-2	Sequence 2, Appl
8	45	8.4	961	5194596-16	Patent No. 5194596
9	45	8.4	961	5219739-16	Patent No. 5219739
10	44.6	8.4	2920	US-09-276-400-1	Sequence 1, Appl
11	44.6	8.4	2920	US-09-448-076-1	Sequence 1, Appl
12	44.6	8.4	2920	US-09-702-572-1	Sequence 1, Appl
13	44.4	8.3	333	US-08-946-026-35	Sequence 35, Appl
14	44.2	8.3	581	US-08-557-309B-22	Sequence 22, Appl
15	44.2	8.3	581	US-08-834-306-22	Sequence 22, Appl
16	44.2	8.3	581	US-08-993-674A-22	Sequence 22, Appl
17	44.2	8.3	581	US-09-256-976-22	Sequence 22, Appl
18	43	8.1	2589	US-08-569-749-1	Sequence 1, Appl
19	43	8.1	2589	US-08-569-749-1	Sequence 1, Appl
20	43	8.1	3238	US-08-123-934A-5	Sequence 5, Appl
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22	42.8	8.0	1332	US-09-057-762-1	Sequence 1, Appl
23	42.8	8.0	1332	US-08-326-119A-1	Sequence 1, Appl
24	42.8	8.0	3471	US-09-002-227-2	Sequence 2, Appl
25	42.6	8.0	1776	US-09-149-476-59	Sequence 59, Appl
26	42	7.9	940	US-08-471-717-1	Sequence 1, Appl
27	42	7.9	2025	US-09-149-476-316	Sequence 316, App

#### ALIGNMENTS

28	42	7.9	2346	4	US-09-149-476-193	Sequence 193, App
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34	41	7.7	218	4	US-09-480-921B-18	Sequence 18, Appl
35	40.8	7.6	1046	1	US-08-361-467B-4	Sequence 4, Appl
36	40.8	7.6	1046	1	US-08-484-332C-4	Sequence 4, Appl
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RESULT 1  
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Sequence 98, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
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EARLIER FILING DATE: 1997-10-02

## Query Match

89.6%; Score 478.6; DB 4; Length 506;

Best Local Similarity 97.4%; Pred. No.36-113;

Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

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QY 517 AAAAAAAAAAAAAAAAAA 533  
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RESULT 3  
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; Sequence 95, Application US/09385982  
; Patent No. 6262334  
; GENERAL INFORMATION:  
; APPLICANT: ENDEGE, WILSON O., ET AL.  
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
; TITLE OF INVENTION: PRODUCTS II  
; FILE REFERENCE: CDNA-260XX  
; CURRENT APPLICATION NUMBER: US/09/385,982  
; EARLIER FILING DATE: 1999-08-30  
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; EARLIER FILING DATE: 1999-06-08  
; EARLIER APPLICATION NUMBER: 60/117,393  
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US-09-385-982-95

Query Match 50.9%; Score 272; DB 4; Length 392;  
Best Local Similarity 95.5%; Pred. No. 1.3e-60;  
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DB 283 NTTAGTTGATCTAAGATTAACATATTTCTGTATTTCTTCAAAAAA 342  
QY 524 AAAAAAAAAA 534  
DB 343 TNAATTTANAA 353

RESULT 4  
US-08-545-196B-10  
; Sequence 10, Application US/08545196B  
; Patent No. 6080577  
; GENERAL INFORMATION:  
; APPLICANT: MELKI, JUDITH  
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE  
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA

COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,196B  
FILING DATE: 19-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FARACI, C. J.  
REGISTRATION NUMBER: 32,350  
REFERENCE/DOCKET NUMBER: 2121-110P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8050  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1582 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-545-196B-10

Query Match 9.4%; Score 50.4; DB 3; Length 1582;  
Best Local Similarity 71.7%; Pred. No. 0.00078;  
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 443 GTTTGAAATTTTATTTACTTTTATTTGATCTAAGATTAACATATTTCTGTATT 502  
DB 1427 GTACTGTTTCTTCTATCTCTATATGTTTAAAGTATAAATAATTTAAATTTT 1486  
QY 503 CTCGCAAAAAAAAAAAAAAAAAAAAAAAAAA 534  
DB 1487 TTTTAAAAAAAAAAAAAAAAAAAAAAAAA 1518

RESULT 5  
US-08-545-196B-12  
; Sequence 12, Application US/08545196B  
; Patent No. 6080577  
; GENERAL INFORMATION:  
; APPLICANT: MELKI, JUDITH  
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE  
; TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,196B  
FILING DATE: 19-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FARACI, C. J.  
REGISTRATION NUMBER: 32,350  
REFERENCE/DOCKET NUMBER: 2121-110P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8050  
TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1582 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-545-196b-12

Query Match  
Best Local Similarity 71.7%; Score 50.4; DB 3; Length 1582;  
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 443 GTTTGTAATTTTAAATTTAGTTTGTGATTAAGTATTAACATATTTCTGAT 502  
DB 1427 GTACGCTTTTTCATCTCTATATGTTTAAAGTATATATATATTTATTTT 1486  
QY 503 CTTCCAAAAA  
DB 1487 TTTTAAAAA

## RESULT 6

US-08-865-297-5  
Sequence 5, Application US/08865297  
Patent No. 6010853

GENERAL INFORMATION:  
APPLICANT: Prasad V.S. Kanteti, Zhaochui Ao, and Stuart F.

TITLE OF INVENTION: The Silva Genes, No. 6010853el Genes Involved in

NUMBER OF SEQUENCES: 12  
CD27-mediated Apoptosis

CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/865,297

FILING DATE: 29-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Silverl, Jean M.

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: DPN-024

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:

LENGTH: 770 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS

LOCATION: 88..612

US-08-865-297-5

Query Match  
Best Local Similarity 61.5%; Score 46.8; DB 3; Length 770;  
Matches 75; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 413 CAGAAAAAGCCTGTCATGAAAAAAGAGTTTGTATTTATTTACTTTTACTTT 472  
DB 628 CAGCACAAGAGTGTTCACACTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687  
QY 473 GATACAGTATTAACATATTTCTGATTTCTTCCAAAAA  
DB 688 CCGAGTAAACAAGTAAATTAACCTTTTATTTTCCAAAAA

QY 533 AA 534  
DB 748 AA 749

## RESULT 7

US-08-890-865A-2  
Sequence 2, Application US/08890865A  
Patent No. 6307019

GENERAL INFORMATION:  
APPLICANT: Constantini, Franklin

APPLICANT: Zeng, Li

TITLE OF INVENTION: AXIN GENE AND USES THEREOF  
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: US

ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,865A

FILING DATE: 10-JUL-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: White, John P

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/54249

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)391-0526

TELEFAX: (212)278-0400

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 3761 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-890-865A-2

Query Match  
Best Local Similarity 67.0%; Score 45.8; DB 4; Length 3761;  
Matches 65; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 438 AAGAGTTTGTATTTATTTATTTACTTTTGTGATGATGATTAACATATTTCT 497  
DB 3662 AATGACTGTACATATTTCTTTCAAGGTAAGTATGATTAATGAAATTAACGTTT 3721

QY 498 GTATCTTCCAAAAA  
DB 3722 TGAACCTTCCAAAAA

## RESULT 8

US-08-890-865A-2  
Sequence 2, Application US/08890865A  
Patent No. 6307019

GENERAL INFORMATION:  
APPLICANT: Tischer, Edmund G.; Abraham, Judith A.; Fiddes, John  
C.; Mitchell, Richard L.

```

      SEQ ID NO 1
      LENGTH: 2920
      TYPE: DNA
      ORGANISM: Homo sapiens
      FEATURE:
        NAME/KEY: CDS
        LOCATION: (143)..(2401)
US-09-276-400-1

Query Match
Best Local Similarity 8.4%; Score 44.6; DB 3; Length 2920;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 444 TTCTGTAATTTTAAATTACTTTTAGTGTTGATACTAGATTTAACAATTTTCGTATTC 503
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2820 TTTTACTATAATATGCTGCTAGTATATTTTATTTTAAATAAGTCTTCTGTGATT 2879

QY 504 TTCCAAAAAAAAAAAAAAAAAAAAAAAA 534
|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2880 CTTCAGAAAAAAAAAAAAAAAAAAAAAAA 2910


RESULT 11
US-09-448-076-1
Sequence 1, Application US/09448076
Patent No. 6300092
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
FILE REFERENCE: MNI-073CP
CURRENT APPLICATION NUMBER: US/09/448,076
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/117,580
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 09/276,400
EARLIER FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
LENGTH: 2920
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (143)..(2401)
US-09-448-076-1

Query Match
Best Local Similarity 8.4%; Score 44.6; DB 4; Length 2920;
Matches 62; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 444 TTCTGTAATTTTAAATTACTTTTAGTGTTGATACTAGATTTAACAATTTTCGTATTC 503
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2820 TTTTACTATAATATGCTGCTAGTATATTTTATTTTAAATAAGTCTTCTGTGATT 2879

QY 504 TTCCAAAAAAAAAAAAAAAAAAAAAAAA 534
|-| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2880 CTTCAGAAAAAAAAAAAAAAAAAAAAAAA 2910


RESULT 12
US-09-702-572-1
Sequence 1, Application US/09702572
Patent No. 6391602
GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
FILE REFERENCE: MNI-073
CURRENT APPLICATION NUMBER: US/09/702,572
CURRENT FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/276,400
PRIOR FILING DATE: 1999-03-25

```

441 AAGTTCGAACTTAACTTTAGTTGATACCAAGTATTAAACATATTTCTGT

APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF

TITLE OF INVENTION:	COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF
NUMBER OF SEQUENCES:	65



## CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle

STATE: Washington  
COUNTRY: USA

ZIP: 98104-7092

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/834,306

FILING DATE: 15-APR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.422C1

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 581 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-834-306-22

## Query Match

8.3%; Score 44.2; DB 3; Length 581;

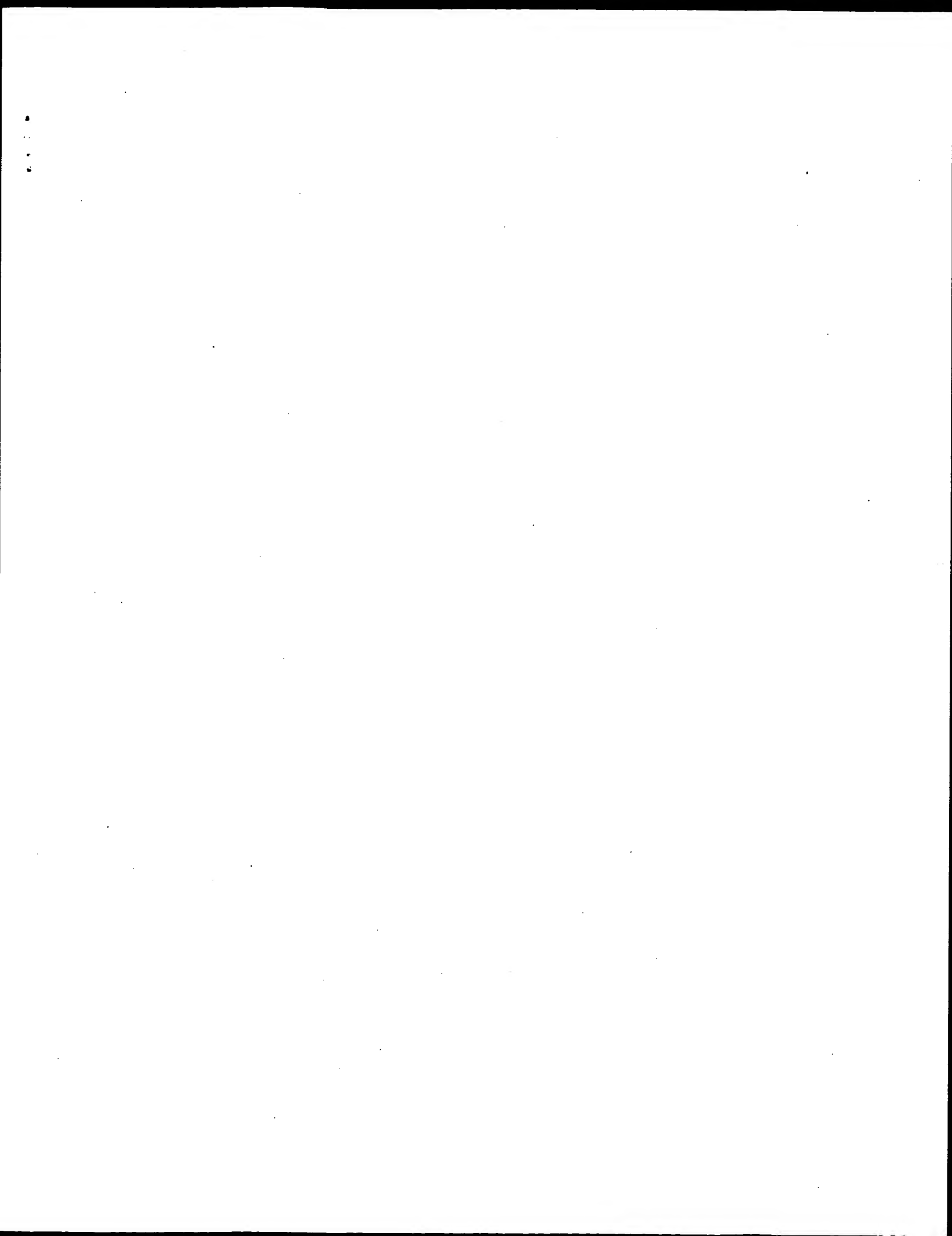
Best Local Similarity 68.5%;

Pred. No. 0.02; Mismatches 28; Indels 0; Gaps 0;

Matches 61; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 446 TTGTAATTTTATATCTTTTGTGATCTAGATTTAACAATTTCTGTATCTT 505  
DB 484 TTTTATTAATAGCTCTTTTATTTATGAGAAGATGCTGTGTTGTTGTTT 543  
QY 506 CCAAAAAAAAAAAAAAAAAAAAAA 534  
DB 544 CAAAAAAAAAAAAAAAAAAAAA 572

Search completed: June 25, 2003, 11:55:46  
Job time : 68 secs





Db	121	GGAAAGTGTGCTGCTGGGTCTGCAGACGGATGATACGTGCGAGCGCAAAATTAATACCA	180
QY	181	TGCCCCCTTCTGTTTAGTGTGAAGAAGCCACGTGAAGATGCTGGCGCTGGATATTATCA	240
Db	181	TCGCCCTTCTGTTTAGTGTGAAGAAGCCACGTGAAGATGCTGGCGCTGGATATTATCA	240
QY	241	CTGACTGTGAACAAACAGTATTCATGCTCATGCTATCTGTGTGGCAGCTGATACAGAAAC	300
Db	241	CTGACTGTGAACAAACAGTATTCATGCTCATGCTATCTGTGTGGCAGCTGATACAGAAAC	300
QY	301	CACAAATTTGACAGTTGGTGGAGGGGTGTTTGACATTGTACACAGATATGCTCTTGC	360
Db	301	CACAAATTTGACAGTTGGTGGAGGGGTGTTTGACATTGTACACAGATATGCTCTTGC	360
QY	361	CGACGGGGCCTTATTATTCGGAACCTCTGTTCAATCCAGCGGCTCTTACCGAGAAAA	420
Db	361	CGACGGGGCCTTATTATTACCGAACCCTCTGTTCAATCCAGCGGCTCTTACCGAGAAAA	420
QY	421	GCCCTGTGCATGAAAAAAGAAGTTTGTAAATTTTAAATTAATCTTTTAGTTGATACTAA	480
Db	421	GCCCTGTGCATGAAAAAAGAAGTTTGTAAATTTTAAATTAATCTTTTAGTTGATACTAA	480
QY	481	GTTTAAACATATTTCTGATCTCTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	534
Db	481	GTTTAAACATATTTCTGATCTCTCCAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	534

## RESULT 2

```

US-10-106-698-1927
: Sequence 1927, Application US/10106698
: Publication No. US20030109690A1
: GENERAL INFORMATION:
:   APPLICANT: Ruben et al.
:   TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
:   FILE REFERENCE: PA005P1
:   CURRENT APPLICATION NUMBER: US/10/106,698
:   CURRENT FILING DATE: 2002-03-27
:   PRIOR APPLICATION NUMBER: PCT/US00/26524
:   PRIOR FILING DATE: 2000-09-28
:   PRIOR APPLICATION NUMBER: US 60/157,137
:   PRIOR FILING DATE: 1999-09-29
:   PRIOR APPLICATION NUMBER: US 60/163,280
:   PRIOR FILING DATE: 1999-11-03
:   NUMBER OF SEQ ID NOS: 8564
:   SOFTWARE: PatentIn Ver. 3.0
:   SEQ ID NO 1927
:   LENGTH: 358
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   NAME/KEY: misc:feature
:   LOCATION: (514)..(514)
:   OTHER INFORMATION: n equals a,t,g, or c
: US-10-106-698-1927

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Query Match	93.1%;	Score 497.2;	DB 9;	Length 558;
Best Local Similarity	98.4%;	Pred. No. 2.2e-115;		
Matches 499; Conservative	2;	Mismatches 6;	Indels 0;	Gaps 0;

QY	16	TGAAGCCGAGCTGGCGGAGAAGTAAAGGAGAGGCGGTGCTCCGCCGCGGTGGCGTTGCTA	75
		:	
		:	
Db	11	TGAGTCGGAGAGCTGGCGAGAAAGTAAGGGAGAGGCGGTGCTCCGCCGCGGTGGCGTTGCTA	70
		:	
QY	76	TGCACTCGAGAGACCCTACTCAGCGAGCGCAAGCTGAGAAAGATTGAGGGGAAAAGTGCTGTGC	135
		:	
Db	71	TGCCTTCGAGAACCTCTACTCAGCGAGCCAGCGCTGAGAAAGATTGAGGGGAAAAGTGCTGTGC	130
		:	
QY	136	TGGGCTTCGAGACGGGATGATGATAAGTCCAGCCGAAAAATAAACAATGCCCTCTCTCTT	195
		:	
Db	131	TGGGCTTCGAGACGGGATGATGATAAGTCCAGCCGAAAAATAAACAATGCCCTCTCTCTT	190
		:	
QY	196	CAGTGTGAAGAGCCACGCTGAAGATCTCGCGCTGGATATTATVCACTCACTGTGAACAC	255

Db 191 CAGGTGMAAGGCACAGTGAAGATCTCGGGCTGGATTTATCAACTCAGTGAAC 250  
 OY 256 AGATTTCATGCTCATTGATCTGTGTGGACGTATACAGAAACCAACATTGACAGT 315  
 Db 251 AGATTTCATGCTCATTGATCTGTGTGGACGTATACAGAAACCAACATTGACAGT 310  
 OY 316 TGGGGAGGGGGTGTGGACCTGTGCAGACGATAGCTGCTTGGCAGAGGGGCCCTAT 375  
 Db 311 TGGTGGAGGGGGTGTGGACCTGTGCAGACGATAGCTGCTTGGCAGAGGGGCCCTAT 370  
 OY 376 TTACCGGAAGCCTCTGTTCAATCCAGGCGTCTTACAGAAAAAGCCTGTGATGAAA 435  
 Db 371 TTACCGGAAGCCTCTGTTCAATCCAGGCGTCTTACAGAAAAAGCCTGTGATGAAA 430  
 OY 436 AAAAGAAAGTTTGTAAATTTATATTACTTTTAACTTAACTAAAGTAATTAATTT 495  
 Db 431 AAAAGAAAGTTTGTAAATTTATATTACTTTTAACTTAACTAAAGTAATTAATTT 490  
 OY 496 CTGATTCCTCCAAAAAAGAAAAA 522  
 Db 491 CTGATTCCTCCAAAAAAGAAAAA 517

### RESULT 3

```

US-09-809-391-98
: Sequence 98, Application US/09809391
: Publication No. US20030049618A1
:
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: 186 Human Secreted proteins
: FILE REFERENCE: P2002p2
: CURRENT APPLICATION NUMBER: US/09/809,391
: CURRENT FILING DATE: 2001-03-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 761
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 98
: LENGTH: 504
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
US-09-809-391-98

```

Query Match	91.1%;	Score 486.6;	DB 9;	Length 504;
Best Local Similarity	99.0%;	Pred. No. 9.8e-113;		
Matches 500; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1

QY	21	CCGAGCTGGGCGGAAAGTGGGGGAGGGGGGAGTCCGCGCGGGGGTGGTATCCGCT	80
Db	1	CCGAGCTGGGCGGAAAGTGGGGGAGGGG-ACGAGCCCCGGGTGGCGGTGCTATCCGT	59
QY	81	TCGCAGAACCTACTAGCGAGCCAGCTGAGGAAGTTGAGGAAAGTGTCTGTGGGT	140
Db	60	TCGCAGAACCTACTAGCGAGCCAGCTGAGGAAGTTGAGGAAAGTGTCTGTGGGT	119
QY	141	CTGCAGACGGATGATGATAACGTGACGCCGAAATTAACATCCGCCCTTGTGTTACAGT	200
Db	120	CTGCAGACGGATGATGATAACGTGACGCCGAAATTAACATCCGCCCTTGTGTTACAGT	179
QY	201	TGAAAGCCACGTGAAAGATGTGCGCGTGGATATTATCACTCACTGTAACAACAGTAT	260
Db	180	TGAAAGCCACGTGAAAGATGTGCGCGTGGATATTATCACTCACTGTAACAACAGTAT	239
QY	261	TCATGTCACTGTAATCTGTGTGGGACATGATACAGAAACACACACTTATACAGTTGGTG	320
Db	240	TCATGTCACTGTAATCTGTGTGGGACATGATACAGAAACACACACTTATACAGTTGGTG	299
QY	321	GAGGGGTGTTTCATCTTGACAGACAGATGCTGTCTTGCGAGAGGGGCCCTTATTATAC	380
Db	300	GAGGGGTGTTTCATCTTGACAGACAGATGCTGTCTTGCGAGAGGGGCCCTTATTATAC	359
QY	381	GGAGCTTCTGTTCAATCCACAGCGTCCCTTACAGAAAAAGCCTGTGCATGAAAAAAG	440

DB	360	GGAGCGTTCTGTCATCCACGGGTCCTTACACGAAAAAGCCTGTGCATGAAAAAAG	419
QY	441	AACTTTTGAAATTTTATTTACTTTTGGTTGATGACTAACTATTAACATTTTCGTA	500
DB	420	AACTTTTGTAATTTTATTTACTTTTGGTTGATGACTAACTATTAACATTTTCGTA	479
QY	501	TTCTTCCAAAAAATTTTTTTTTT	525
DB	480	TTCTTCCAAAAAATTTTTTTTTT	504

RESULT 4  
US-09-80

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; Sequence 252, Application US/09809391
; Publication No. US20030049618A1
;
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 166 Human Secreted proteins
; FILE REFERENCE: P2002p2
; CURRENT APPLICATION NUMBER: US/09/809,391
; PRIORITY FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 252
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-252

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Query Match	89.68;	Score 478.6;	DB 9;	Length 506;
Best Local Similarity	97.48;	Pred. No. 1e-110;		
Matches 484; Conservative	2;	Mismatches 11;	Indels 0;	Gaps 0;

OY		37	GTAAGGGAAGGGCGGTCTCCGCCGGCGGTGGCGGTTCATATCGCTTCCGACAACTACTCA	96
Dd		2	GCACGATTTTGGCAGGACCSCCGCGGTGGCGGTTCATATCGCTTCCGACAACTACTCA	61
OY		97	GGCAGCCAGCTGAGAAGAGTTGAGGAAAAGTGCTGCTGGTGGTTCGACAGCGGATGGA	156
Dd		62	GGCAGCCAGCTGAGAAGAGTTGAGGAAAAGTGCTGCTGGTGGTTCGACAGCGGATGGA	121
OY		157	TAAAGTCACCCGAAAAATAAATCGCCCCCTTTCGCTCATGTGTGAAAAGCCACAGTAA	216
Dd		122	TAAAGTCACCCGAAAAATAAATCGCCCCCTTTCGCTCATGTGTGAAAAGCCACAGTAA	181
OY		217	GATCCTCGCGGTGGATTTATCAACTCACTGTGTAACAACAGTATTCATGCTCATCGTATC	276
Dd		182	GATCCTCGCGGTGGATTTATCAACTCACTGTGTAACAACAGTATTCATGCTCATCGTATC	241
OY		277	TGTGTGGCACATATACCAAAAACCAACATTGACAGTGGTGGAGGGGGTGTTCACACT	333
Dd		242	TGTGTGTGGCACATATACCAAAAACCAACATTGACAGTGGTGGAGGGGGTGTTCACACT	301
OY		337	TGTGACAGCAGTATGCTGTCTTGCACACGGGGCCCTATTATACCGAAGCTTCGTCCAA	396
Dd		302	TGTGACAGCAGTATGCTGTCTTGCACACGGGGCCCTATTATACCGAAGCTTCGTCCAA	361
OY		397	TCCCAGCGGTCCTTACACAAAAAGCCTGTGCATGAAAAAAAAGAAAGTTTGTATTTTA	455
Dd		362	TCCCAGCGGTCCTTACACAAAAAGCCTGTGCATGAAAAAAAAGAAAGTTTGTATTTTA	421
OY		457	TATTAAGTTTTAGTTGATTAAGTAAATTAACATATTTCTGTATTTCTCCAAAAAAA	516
Dd		422	TATTAAGTTTTAGTTGATTAAGTAAATTAACATATTTCTGTATTTCTCCAAAAAAA	481
OY		517	AAAAAAAAAAAAAAAAAAAA 533	
Dd		482	AAAAAAAAAAAAAAAAAAAA 498	

RESULT 5  
US-09-918-995-19489

```

? Sequence 19489, Application US/09918995
? Publication No. US20030073623A1
? GENERAL INFORMATION:
? APPLICANT: Hyseq, Inc.
? TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
? TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
? FILE REFERENCE: 20411-756
? CURRENT APPLICATION NUMBER: US/09/918,995
? CURRENT FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: US/09/235,076
? PRIOR FILING DATE: 1999-01-20
? NUMBER OF SEQ ID NOS: 38054
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 19489
? LENGTH: 512
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(512)
? OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19489

```

Query Match	86.2%;	Score 460.2;	DB 9;	Length 512;
Best Local Similarity	99.1%;	Pred. No. 4.3e-106;		
Matches 462;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

QY	57	ACCGCGGGGGGTTGGTATGCGTTCCGAGAAACCTACTCAGGACGCGAGCAAGT	116
Db	47	GCCGGGGGGGGTGTCTATCGCTTCGAGAACTCTACAGGACGCCAGCTGAGAAAGT	106
QY	117	TGAGGAAAGTGTCTGCTGCTGGGTCTGCAGACGGGATGATTAAGTGCAGCCGAAATTA	176
Db	107	TGAGGAAAGTGTCTGCTGCTGGGTCTGCAGACGGGATGATTAAGTGCAGCCGAAATTA	166
QY	177	AACTGCGCCCTTCTGCTTCACTGTGAAGGCGACGTAAGATGCTGGCGGTGATTA	236
Db	167	AACATCGCCCTTCTGCTTCACTGTGAAGGCGACGTAAGATGCTGGCGGTGATTA	226
QY	237	TCAATCACTGGTAAACAACAGTATTCATGCTCATCTGATTCGTGTGTGGCACTGATACCG	296
Db	227	TCAATCACTGGTAAACAACAGTATTCATGCTCATCTGATTCGTGTGTGGCACTGATACCG	286
QY	297	AAACCAACAATTCAGACTGTGGAGGGGTGTGGCACTGTGTGACACACTATATGCTGC	356
Db	287	AAACCAACAATTCAGACTGTGGAGGGGTGTGGCACTGTGTGACACACTATATGCTGC	346
QY	357	TTGCCGAGGGGCCCTTATTTAACCGGAGCTCTCTTAATCCGACGGCTCTTACCGAGA	416
Db	347	TTGCCGAGGGGCCCTTATTTAACCGGAGCTCTCTTCAATCCGACGGCTCTTACCGAGA	406
QY	417	AAAGCCGTGTGCATGAAAAAAGAGTGTGTGAATTTTATATTATCTTTTAGTTGATA	476
Db	407	AAAGCCGTGTGCATGAAAAAAGAGTGTGTGAATTTTATATTATCTTTTAGTTGATA	466
QY	477	CTAAGTATTAACATATTCGTATCTCTCCAAAAAATTTTTTTTTT	522
Db	467	CTAAGTATTAACATATTCGTATCTCTTTTTAAAAAAAAAAAAAAAA	512

RESULT 6  
US-09-822-846-397  
Sequence 397, Application US/09822846A  
Publication No. US20030027139A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavalie, Edward R.  
APPLICANT: Collins-Reicle, Lisa A.  
APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Agostino, Michael J.

Query Match	79.68;	Score 425;	DB 9;	Length 439;
Best Local Similarity	99.88;	Pred. No. 2.8e-97;		
Matches 436;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1.

RESULT 7  
US-09-918-995-6534

Sequence 6534, Application US/09918995  
Publication No. US20030073623A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
FILE REFERENCE: 20411-756  
CURRENT APPLICATION NUMBER: US/09/918, 995  
CURRENT FILING DATE: 2001-07-30

Query Match	75.7%;	Score 404;	DB 9;	Length 422;
Best Local Similarity	100.0%;	Pred. No. 5.3e-92;		
Matches 404; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

RESULT 8  
HC-00-07

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; Sequence 189, Application US/09978295A
; Patent No. US20020156006A1
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APPLICANT:	Ashkenazi, Avi
APPLICANT:	Baker Kevin P.
APPLICANT:	Bostein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Eaton, Dan
APPLICANT:	Ferrara, Napoleon
APPLICANT:	Filtaroff, Ellen
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gedder, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J
APPLICANT:	Kiljavin, Ivar J.
APPLICANT:	Kuo, Sophia S.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pan, Jamesi
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Shelton, David L.
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunias, Daniel

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7% Score 335; DB 9; Length 663;  
Best Local Similarity 76.0% Pred. No. 1,6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

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82 GCGAGACCTACTGAGGAGCGGAGAGTAGAGGGGCGGCTGCGCTATCGCTT 141  
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121 TGCAGACGCGATGATTAACGTGACCGGAGAGTAGAGGGGCGGCTGCGCTATCGCTT 180  
202 GAAAGCGGAGGAGAGTAGAGGGGCGGCTGCGCTATCGCTTATCGCTTAT 229  
191 GAAAGCGGAGGAGAGTAGAGGGGCGGCTGCGCTATCGCTTATCGCTTAT 240  
230 ----- 229  
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230 ----- 229  
301 ATTTTCATACCTTTATATGATCTACAGCTTATGATGATTAATGAAGTGTATTTGGCC 360  
230 -----GATATTTATCACTCAGTGTGACAGAGTATTCATGCTCATGATGCTT 282  
361 TTTCGCTGATATTTATCACTCAGTGTGACAGAGTATTCATGCTCATGATGCTT 420  
283 GGCAGCTGATTAACAGAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 342  
421 GGCAGCTGATTAACAGAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 480  
343 AGCAGTATGCTGCTTGGCGAGGCGGCTTATTTACCGAGAGTGTGACAGAGTGTGAC 402  
481 AGCAGTATGCTGCTTGGCGAGGCGGCTTATTTACCGAGAGTGTGACAGAGTGTGAC 540  
403 CGGCTCTTACAGAGAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 462  
541 CGGCTCTTACAGAGAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 600  
463 TTTTACGCTGATTAACAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 522  
TTTTTACGCTGATTAACAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC

Db 601 TTTTACGCTGATTAACAGAGTGTGACAGAGTGTGACAGAGTGTGACAGAGTGTGAC 660  
QY 523 AAA 525  
Db 661 AAA 663  
RESULT 9  
US-09-978-697-189  
Sequence 189, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavrin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paul, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978, 697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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Query Match 62.7% Score 335 DB 9; Length 663;  
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Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

QY 22 CGAGCTGGCGAGAGTGGGGAGGCGGTCTCCGCGCGGTGGCGGTCTATCGCTT 81  
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QY 523 AAA 525  
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RESULT 10  
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; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Ferrara, Napoleon  
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; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978, 192A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;  
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

22 CGAGCTGGGGCGAAGTAGGAGGGGCGGCTGCGCGCGGCGGCTGCTATCGCTT 81  
1 CGAGCTGGGGCGAAGTAGGAGGGGCGGCTGCGCGCGGCGGCTGCTATCGCTT 60  
82 CGCAGACCTACTCAGCAGCCAGCTGAGAGTTGAGGAGAAAGCTGCTGCTGCTG 141  
61 CGCAGACCTACTCAGCAGCCAGCTGAGAGTTGAGGAGAAAGCTGCTGCTGCTG 120  
142 TGCAGACCGGATGATACGTGACCCGCAATAAATGCGCCCTGCTGCTGCTGCT 201  
121 TGCAGACCGGATGATACGTGACCCGCAATAAATGCGCCCTGCTGCTGCTGCT 180  
202 GAAAGGCCACGTGAGATGCTGCGGCTG----- 229  
181 GAAAGGCCACGTGAGATGCTGCGGCTGCACTGACATCTATGACCTTTTAT 240  
230 ----- 229  
241 CATCGCAAGCCCTGAGACCATATATGTTATCACTGATTTGAAGTACCGTTATCT 300  
230 ----- 229  
301 ATTTTCATCTTTATATGCTACTGACCTGATGATTAAGATGTTATTTGGCC 360  
230 -----GATATTATCACTCACTGTAACAACAGTATTCATGCTATGCTGTT 282  
361 TTTCGTTGATATTAATCACTCACTGTAACAACAGTATTCATGCTATGCTGTT 420  
283 GGCACGTGATACCAAGAACCAACAACATGACATTTGTTGAGGGGTTTGCACCTGTGC 342  
421 GGCACGTGATACCAAGAACCAACAACATGACATTTGTTGAGGGGTTTGCACCTGTGC 480  
343 AGCAGTATGCTGCTGCGGAGGGGCTTATTAACGGAAGCTTCTGTTCAATCCAG 402  
481 AGCAGTATGCTGCTGCGGAGGGGCTTATTAACGGAAGCTTCTGTTCAATCCAG 540  
403 CGGTCCTTACCAAGAACCTGTCATGATAAAGATTTTGTATTTATATATAC 462  
541 CGGTCCTTACCAAGAACCTGTCATGATAAAGATTTTGTATTTATATATAC 600  
463 TTTTACGTTGATGATGATGATTAACATATTTCTGATTTCCAAAAA 522

Db 601 TTTTAGTTGACTACTATTAACATATTCTGTATCTTCCAAAAA 660  
Oy 523 AAA 525  
Db 661 AAA 663

## RESULT 11

US-09-999-832A-189  
Sequence 189, Application US/0999832A  
Publication No. US20020192706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Klavins, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C63  
CURRENT APPLICATION NUMBER: US/09/999, 832A  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1, 6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

Qy 22 CGAGCTGGGCGAGAACTAGGAGGCGGCTCCCGCGGAGGCGGTTGCGATGCGTT 81  
Db 1 CGAGCTGGGCGAGAACTAGGAGGCGGCTCCCGCGGAGGCGGTTGCGATGCGTT 60

Qy 82 CGCAGAACTTACTAGGACCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGTC 141  
Db 61 CGCAGAACTTACTAGGACCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGTC 120  
Qy 142 TGCAGACGCGATGATTAAGTGCAGCCGAAATTAACATCGCCCTTCTGCTGAGTGT 201  
Db 121 TGCAGACGCGATGATTAAGTGCAGCCGAAATTAACATCGCCCTTCTGCTGAGTGT 180  
Qy 202 GAAAGCGCAGTGAAGTGTGCGGCTG----- 229  
Db 181 GAAAGCGCAGTGAAGTGTGCGGCTGCGACTAAGTGTGATGATGACCTTTTAT 240  
Qy 230 ----- 229  
Db 241 CATGCGAAGCCCGTGAACCATATATTTATCACTGATTTGAATGACCGTATCTT 300  
Qy 230 ----- 229  
Db 301 ATTTTCATCTTTTATATGACTCAGACTGATTCATTAATGAACTGTTATTTGGCC 360  
Qy 230 -----GATATTAATCACTCACTGTAACAGATTCATGCTCATGCTGTT 282  
Db 361 TTTCCTGATTTATCACTCACTGTAACAGATTCATGCTCATGCTGTT 420  
Qy 283 GGCAGTATACCAAGAAACCAACATTTGAGAGGCGGTTGCACTGTGAC 342  
Db 421 GGCAGTATACCAAGAAACCAACATTTGAGAGGCGGTTGCACTGTGAC 480  
Qy 343 AGCAGTATGCTGTTGCGAGCGGCTTATTTACCGAAGCTGCTGTAATCCAG 402  
Db 481 AGCAGTATGCTGTTGCGAGCGGCTTATTTACCGAAGCTGCTGTAATCCAG 540  
Qy 403 CGTCTTACCAAGAAAGCTGCTGTAAGAAAGAGTTTGAATTTATATTTAC 462  
Db 541 CGTCTTACCAAGAAAGCTGCTGTAAGAAAGAGTTTGAATTTATATTTAC 600  
Qy 463 TTTTGAATGATTAAGTATTAACATTTTCTGATTTCTTCCAAAAA 522  
Db 601 TTTTGAATGATTAAGTATTAACATTTTCTGATTTCTTCCAAAAA 660  
Qy 523 AAA 525  
Db 661 AAA 663

RESULT 12  
US-09-978-189-189  
Sequence 189, Application US/09978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Borstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-05-15  
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

22 CGAGCTGGGCGAAGAGTGGGAGGCGGCTGCTCCGCGGCGGCTGCTGCTT 81  
1 CGAGCTGGGCGAAGAGTGGGAGGCGGCTGCTCCGCGGCGGCTGCTGCTT 60  
82 CGCAGACCTACTCTAGGAGGCGGAGTGGGAGGAGTGGGAGGAGTGGGAGG 141  
61 CGCAGACCTACTCTAGGAGGCGGAGTGGGAGGAGTGGGAGGAGTGGGAGG 120  
142 TGCAGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201  
121 TGCAGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
202 GAAAGGCCAGTGAAGATGCTGCGGCTG----- 229  
181 GAAAGGCCAGTGAAGATGCTGCGGCTGCGCACTGATGATGATGATGATGAT 240  
230 ----- 229  
241 CATCGCAGAGCCCTGAACCATATATTTTATCTCACTGATGATGATGATGAT 300  
230 ----- 229  
301 ATTTTCACTTTTATATGATGATGATGATGATGATGATGATGATGATGATG 360  
230 -----GATATTATCACTCTGCTGATGATGATGATGATGATGATGATGAT 282  
361 TTTGCTGATATATCACTCTGCTGATGATGATGATGATGATGATGATGATG 420  
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421 GGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
343 AGCAGTATGCTGCTTGGCGAGCGGCGCTTATTTACCGAGCTTCTGTTCAAT 402  
481 AGCAGTATGCTGCTTGGCGAGCGGCGCTTATTTACCGAGCTTCTGTTCAAT 540  
403 CGGCTCTTACGAGAGAGCTGCTGATGATGATGATGATGATGATGATGATG 462  
541 CGGCTCTTACGAGAGAGCTGCTGATGATGATGATGATGATGATGATGATG 600

463 TTTTACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522  
601 TTTTACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

523 AAA 525  
661 AAA 663

RESULT 13

US-09-978-608A-189  
Sequence 189, Application US/09978608A  
Publication No. US20030045462A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Williams, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C22  
CURRENT FILING DATE: 2001-10-16  
NUMBER OF SEQ ID NOS: 624  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 189  
LENGTH: 663  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-978-608A-189

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;

Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

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82 CGCAGACCTACTCTAGGAGGCGGAGTGGGAGGAGTGGGAGGAGTGGGAGG 141  
61 CGCAGACCTACTCTAGGAGGCGGAGTGGGAGGAGTGGGAGGAGTGGGAGG 120  
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PRIOR APPLICATION NUMBER:	60/081229



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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.7%; Score 335; DB 9; Length 663;  
Best Local Similarity 76.0%; Pred. No. 1.6e-74;  
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

22 CGAGCTGGCGAAGAGGAGGCGGCTCCCGCGGCGGCTGCTATGCT 81  
1 CGAGCTGGCGAAGAGGAGGCGGCTCCCGCGGCGGCTGCTATGCT 60  
82 CGCAGAACCTACTCAGGCGAGCGAGTGAAGAGTTGAGGAGAAAGTGTCTGCTGGTC 141  
61 CGCAGAACCTACTCAGGCGAGCGAGTGAAGAGTTGAGGAGAAAGTGTCTGCTGGTC 120  
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230 ----- 229  
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283 GGCACGATACCAAGAAACCAACATGACAGTTGGAGGGGTGTTGCACTTGTGAC 342  
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403 CGGTCCTTACCAAGAAAGCTGTCATGAAAAAAGAGTTTGAATTTATATTTAC 462  
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463 TTTTATTTGATTAAGTATTAACATTTTCTGATTTCTTCAAAAAA 522  
601 TTTTATTTGATTAAGTATTAACATTTTCTGATTTCTTCAAAAAA 660  
523 AAA 525  
661 AAA 663

RESULT 15  
US-09-978-403A-189

Sequence 189, Application US/09978403A  
Publication No. US20030050240A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Flvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James:  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/066364  
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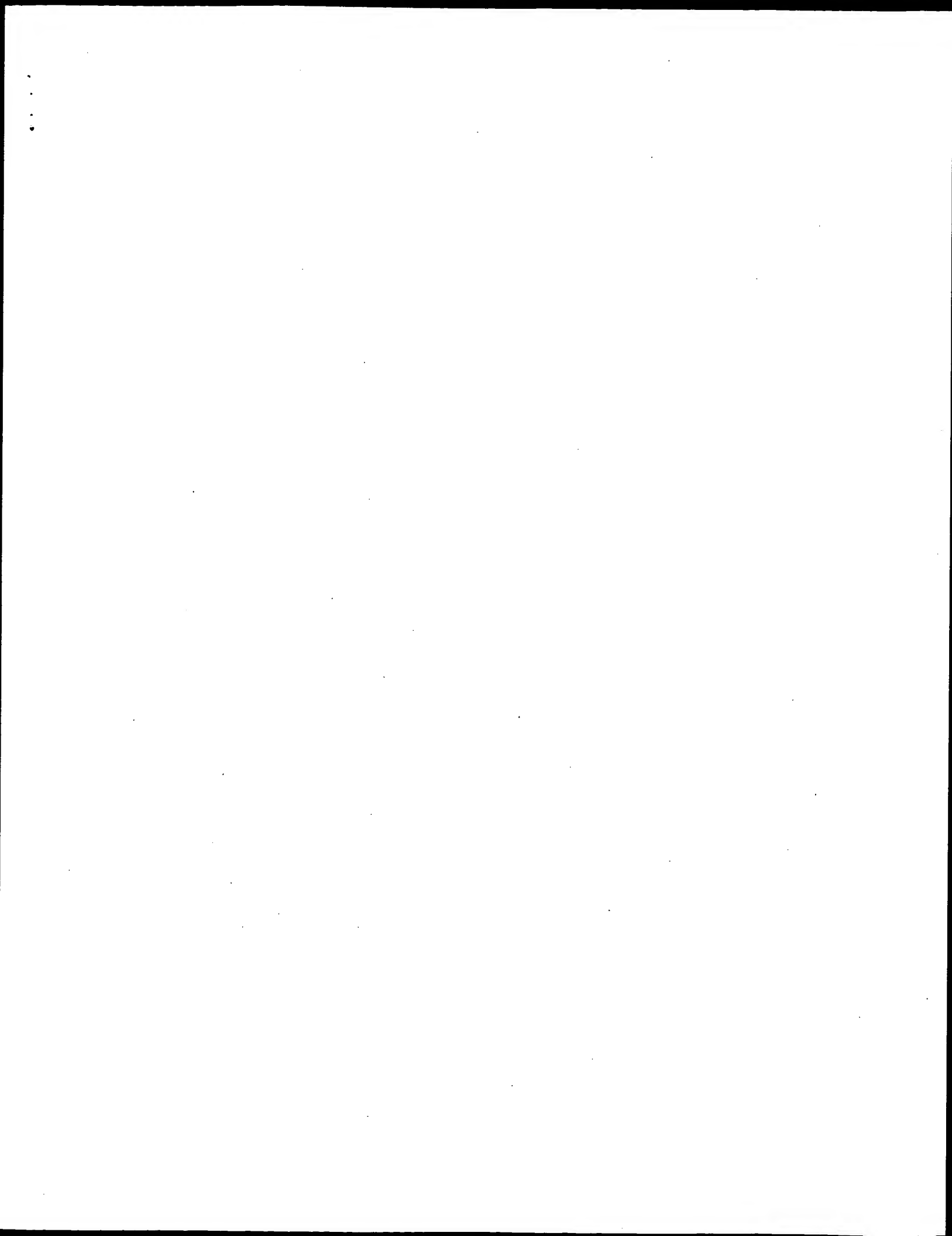
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 PRIOR APPLICATION NUMBER: 60/084640  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084598  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084643  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match	62.7%;	Score 335;	DB 9;	Length 663;
Best Local Similarity	76.0%;	Pred. No. 1.6e-74;		
Matches 504;	Conservative	0;	Mismatches 0;	Indels 159;
				Gaps 1

QY 22 GAGATGGGCGGAGTATGGGGAGGCGCGTGTCCGCGCGGTGGCGGTTTGGTATACGGCTT 81  
 Db 1 CGAGTGGGCGGAGAGTGGGAGGCGCGGTCTCCGCGCGGTGGCGGTTTGGTATACGGCTT 60  
 QY 82 CGCAGACCTTACTCAGGCAGCCAGCTGAGAGAGTTTGAGGGAAAGTGTGCTGTGGCTG 141  
 Db 61 CGCAGACCTTACTCAGGCAGCCAGCTGAGAGAGTTTGAGGGAAAGTGTGCTGTGGCTG 120  
 QY 142 TGCAGACGGGATGGATTAACGTGCACGCCGGAATAAACAATCCGCCCTTTGTGCTTCAGTGT 201  
 Db 121 TGCAGACGGGATGGATTAACGTGCACGCCGGAATAAACAATCCGCCCTTTGTGCTTCAGTGT 180  
 QY 202 GAAAGGCCACGTGAAGATGCTGGCGCTG----- 229

Db	181	GAAGGCCACAGTGAAGATCTGCGGCTGGCACTAACCTGTGACATCTAAGACCTTTTAA	240
OY	230	-----	229
Db	241	CATGCGACAAGCCCTGGAACATATATGTTATCATCTGGATTGGAAGTCAACCGTTATCTT	300
OY	230	-----	229
Db	301	ATTTTCATACCTTTTATATGTACTGAGACTGATGCGATTATGAAGTGTTATTTGGCC	360
OY	230	-----	282
Db	361	TTTGCTTGAATATATATCACTCACTGTTAAACAACATATTCATGCTCATCGATCTGTT	420
OY	283	GGACAGTATACCGAAGAACACAAACATGTGACATTTGGTGGAGGGGTGTTGCATCTGGAC	342
Db	421	GGACCTGATACCGAAGAACACAAACATTTGACACTTGTGTAGAGGGTGTTCATCTGGAC	480
OY	343	AGCAGTATGCTGTCTTGGCGAGCGGGCCCTTATTTTACCGGAAGCTCTGTCAATCCAG	402
Db	481	AGCAGTATGCTGTCTTGGCGAGCGGGCCCTTATTTTACCGGAAGCTCTGTCAATCCAG	540
OY	403	CGGTCCTTACCAAAAAAGCTGTGTGATGAAAAAAAGATTTGTATTTATTTAC	462
Db	541	CGGTCCTTACCAAAAAAGCTGTGTGATGAAAAAAAGATTTGTATTTATTTAC	600
OY	463	TTTTTACTTGATCTAGTATTTAAACATATTTCTGTATTTCTCCAAAAA	522
Db	601	TTTTTACTTGATCTAGTATTTAAACATATTTCTGTATTTCTCCAAAAA	660
OY	523	AAA 525	
Db	661	AAA 663	

Search completed: June 25, 2003, 12:47:19  
Job time : 143 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 07:52:21 ; Search time 1418 Seconds

(without alignments)  
6099.006 Million cell updates/sec

Title: US-09-801-115b-1

Perfect score: 534  
Sequence: 1 gtcccaatctgaatgaag.....aaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505.8	94.7	524	12	BG705303
2	492.4	92.2	962	12	BG248994
3	491.8	92.1	510	12	BF399486
4	487	91.2	781	13	BG529072
5	485.4	90.9	487	13	BM472086
6	482.4	90.3	534	12	BG031757

7	468.2	87.7	529	12	BF691818
8	468	87.6	468	12	BE109912
9	467.6	87.6	930	12	BE203359
10	452	84.6	452	9	AT078580
11	445	83.3	453	9	AT743235
12	432.4	81.0	533	10	AV754613
13	430.4	80.6	432	9	AA429945
14	427	80.0	427	9	AA455042
15	422	79.0	423	9	AI128804
16	415.2	77.8	443	12	BG613984
17	413.8	77.5	432	10	AV759888
18	412.4	77.2	543	12	BG532587
19	403	75.5	815	12	BE215121
20	402.6	75.4	409	9	AI826623
21	400.4	75.0	404	13	BM553628
22	399.4	74.8	402	9	AI89747
23	399	74.7	399	9	AA516431
24	394.4	73.9	396	10	AM183193
25	391	73.2	391	9	AI989739
26	386	72.3	386	9	AA911088
27	384.4	72.0	386	9	AA989129
28	381	71.3	395	9	AI141284
29	374.4	70.1	468	14	W52820
30	363	68.0	522	14	W38899
31	361.6	67.7	389	9	AA305052
32	357.6	67.0	456	12	BE875161
33	353	66.1	353	9	AI265924
34	349.4	65.4	692	11	AF151058
35	337.6	63.2	409	14	N89912
36	337.2	63.1	380	9	AA477156
37	331.4	62.1	533	9	AA987264
38	331.4	62.1	583	14	BC013860
39	329.8	61.8	789	12	BE737159
40	327.6	61.3	381	9	AA644621
41	326.2	61.1	331	12	BF388158
42	324.4	60.7	326	9	AI263361
43	324	60.7	325	9	AI371387
44	319.4	59.8	678	13	BI561562
45	319	59.7	319	9	AI349474

#### ALIGNMENTS

RESULT 1  
LOCUS BG705303 524 bp mRNA linear EST 07-MAY-2001  
DEFINITION 602687808F1 NIH\_MGC\_95 Homo sapiens CDNA clone IMAGE:4820568 5',  
mRNA sequence.  
ACCESSION BG705303  
VERSION BG705303.1 GI:13979504  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE 1 (bases 1 to 524)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihai  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM10725 row: 0 column: 01  
High quality sequence stop: 521.  
Location/Qualifiers

#### FEATURES



LOCUS	BF399486	510 bp	RNA	linear	EST 27-NOV-2000
DEFINITION	U1-R-CAL-bjb-b-12-0-UI.s1 U1-R-CAL Rattus norvegicus cDNA clone				
ACCESSION	BF399486				
VERSION	BF399486.1 GI:11384494				
KEYWORDS	EST.				
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 510)				
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.				
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery				
JOURNAL	Genome Res. 6 (3), 791-806 (1996)				
MEDLINE	97044477				
COMMENT	Contact: Soares, MB				

Email: mscoares@blue.woeg.uiowa.edu  
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares lab clone distribution: clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com))  
Seq primer: M13 Forward  
POLYA-yes.

FEATURES	SOURCE	LOCATION/QUALIFIERS
1.	510	
		/organism="Rattus norvegicus"
		/strain="Sprague-Dawley"
		/db_xref="taxon:10116"
		/clone="UI-R-CAL-bjb-b-12-0-UI"
		/clone_id="UI-R-CAL"
		/lab_host="DH10B (Life Technologies)"
		/note="Vector: pUT3D-Pac (Pharmacia) with a modified
		polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-CAL
		library is a subcloned library derived from the following
		tissues: thalamus, cerebellum, hypothalamus, medulla, pons,
		midbrain, cerebral cortex, corpus striatum, testis, and
		hippocampus. For a detailed description of the library
		from which this clone was derived, please visit our web
		site at <a href="http://ratseq.eng.uiowa.edu">ratseq.eng.uiowa.edu</a> . The subtraction has been
		previously described in (Bonaldo, Lennon and Soares,
		Genome Research 6:791-806, 1996)
		TAG_SEQ=None found"
BASE COUNT	130 a	131 c 104 g 145 t
ORIGIN		

	Query Match	Match Similarity	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
	28	92.1%	99.6%	493	0	2	0	0
QY	28	92.1%	99.6%	493	0	2	0	0
DB	495	92.1%	99.6%	493	0	2	0	0
QY	88	92.1%	99.6%	493	0	2	0	0
DB	435	92.1%	99.6%	493	0	2	0	0
QY	148	92.1%	99.6%	493	0	2	0	0
DB	375	92.1%	99.6%	493	0	2	0	0
QY	208	92.1%	99.6%	493	0	2	0	0
DB	315	92.1%	99.6%	493	0	2	0	0

QY	268	CATGTAATCTGTGGCAGCTGATACCAAGAAACCAACATTTGACAGTTGGTGGAGGGGT	327
Db	255	CATGTAATCTGTGGCAGCTGATACCAAGAAACCAACATTTGACAGTTGGTGGAGGGGT	196
QY	328	GTTTGCACTTGTGACAGAGATGATCTGTCTTCCGACGGGGCCCTTATTTACCGGAAAGCT	387
Db	195	GTTTGCACTTGTGACAGAGATGATCTGTCTTCCGACGGGGCCCTTATTTACCGGAAAGCT	136
QY	388	TCTGTCAATCCGACGGGCTCTTACCGAAGAAAACGCTGTGCATGAAAAAAAAGAAGTTT	447
Db	135	TCTGTCAATCCGACGGGCTCTTACCGAAGAAAACGCTGTGCATGAAAAAAAAGAAGTTT	76
QY	448	GTAATTTATATTACTTTTAGTTTGATTAAGTATTTAAACATATTTCTGTATTTCTCC	507
Db	75	GTAATTTATATTACTTTTAGTTTGATTAAGTATTTAAACATATTTCTGTATTTCTTAA	16
QY	508	AAAAAAAAAAAAAA 522	
Db	15	AAAAAAAAAAAAAA 1	

RESULT	4			
B6529072				
LOCUS		781 bp	mRNA	linear EST 03-APR-2001
DEFINITION	B6529072	602557916bp1 NIH_MGC_60 Homo sapiens CDNA clone IMAGE:4713305 5',		
		mRNA sequence.		
ACCESSION	B6529072			
VERSION	B6529072.1	GI:13520609		
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 781)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1992)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: DCTD/BNP CNA Library Preparation: CLONETECH Laboratories, Inc. CNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHC1556 row: 1 column: 18 High quality sequence scop: 4/5. Location/Qualifiers 1..781
FEATURES	
SOURCE	

Query Match	Score 487;	DB 12;	Length 781;
Best Local Similarity	98.7%;	Pred No. 3.7e-63;	
BASE COUNT	228 a	157 c	233 g 163 t
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4713305" /clone_1ib="NIH_MGC_60" /tissue_type="adenocarcinoma" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: prostate; Vector: pDMR-riB (Clontech); Site_1: SfiI (ggccgcctgcgc); Site_2: SfiI (ggccatattgccc ); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATATTGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGGGCGGAGGGGCGGACATG-drr(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies for contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."		





found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM1089 row: e column: 06  
High quality sequence stop: 446.

## FEATURES

source

Location/Qualifiers

1..534

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4394093"

/clone\_lib="NIH\_MGC\_87"

/tissue\_type="mammary adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: breast; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; Oligo-dT primed.

Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

BASE COUNT 163 a 108 c 132 g 131 t  
ORIGIN

## Query Match

Best Local Similarity 98.3%; Score 482.4; DB 12; Length 534;  
Matches 499; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

OY 30 GCGAAGACTAGGAGGCGGCTCCGCCGCGGCTGCGTTCATCGCTTCGACAGAC 89  
DB 1 GCGAAGAGTAGGAGGCGGCTCCGCCGCGGCTGCGTTCATCGCTTCGACAGAC 60  
OY 90 CTACTACGGCAGCAGCTGAGAAAGATTGAGGAGAAATGCTGCTGCTGCTGCTCAACG 149  
DB 61 CTACTACGGCAGCAGCTGAGAAAGATTGAGGAGAAATGCTGCTGCTGCTGCTCAACG 120  
OY 150 CGATGATTAACGTCAGCCGCAAAATTAACATCCGCCCTTCTGCTCAGTGTGAAGGCC 209  
DB 121 CGATGATTAACGTCAGCCGCAAAATTAACATCCGCCCTTCTGCTCAGTGTGAAGGCC 180  
OY 210 ACGTGAAGATCTCGCGCTGATTTATCACTACGTCAGTGTGAAGATTCATGCTCA 269  
DB 181 ACGTGAAGATCTCGCGCTGATTTATCACTACGTCAGTGTGAAGATTCATGCTCA 240  
OY 270 TCGATCTGCTGTCAGCTGATACAGAAACACAACTGATGAGTGGAGAGGGTGT 329  
DB 241 TCGATCTGCTGTCAGCTGATACAGAAACACAACTGATGAGTGGAGAGGGTGT 300  
OY 330 TTGCACTTGTGACAGCAGTATGCTGTGCGCAGCGGGCCCTTATTACCGAAGCTTC 389  
DB 301 TTGCACTTGTGACAGCAGTATGCTGTGCGCAGCGGGCCCTTATTACCGAAGCTTC 360  
OY 390 TGTTCATCCAGCGGCTCTTACAGAAAAAGCCTGTGCAATGAAAAAGAGTTTGT 449  
DB 361 TGTTCATCCAGCGGCTCTTACAGAAAAAGCCTGTGCAATGAAAAAGAGTTTGT 420  
OY 450 AATTTTATTTACTTTTATTTAGTTGATTAAG--TATTAACATATTTCTGATTTCTTC 506  
DB 421 AATTTTATTTACTTTTATTTAGTTGATTAAGTTATTAAACATATTTCTGATTTCTTC 480  
OY 507 CAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 534  
DB 481 CAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 508

## RESULT 7

BF691818

LOCUS BF691818 529 bp mRNA linear EST 22-DEC-2000  
DEFINITION 60224787F1 NIH\_MGC\_62 Homo sapiens cDNA clone IMAGE:4333244 5',

mRNA sequence.

ACCESSION BF691818

VERSION BF691818.1 GI:11977226

KEYWORDS

SOURCE

ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 529)  
NIH-MGC http://imgc.ncbi.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov

## COMMENT

Tissue Procurement: ATCC/DC/DTP

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC1M200 row: m column: 21

High quality sequence stop: 483.

## FEATURES

source

1..529

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4333244"

/clone\_lib="NIH\_MGC\_62"

/tissue\_type="melanotic melanoma, high MDR"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site\_1:

sfiI (ggcgccctggcc); Site\_2: sfiI (ggccatcagcc);

Double-stranded cDNA was prepared from cell line RNA. 5'

and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CAGGCGCATATGACC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGCGAGGCGGCGGCGGCTGCTATGCTTC

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA)."

BASE COUNT 139 a 119 c 138 g 133 t  
ORIGIN

## Query Match

Best Local Similarity 98.7%; Score 468.2; DB 12; Length 529;  
Matches 484; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

OY 23 GACCTGGGCGAAGATGAGGAGGCGGCTCCGCCGCGGCTGCTATGCTTC 82  
DB 2 GACCTGGGCGAAGATGAGGAGGCGGCTCCGCCGCGGCTGCTATGCTTC 61  
OY 83 GCAGAACCTACTAGCAGCAGCAGTGAAGAAGTTGAGGAAAGTCTGCTGGGCT 142  
DB 62 GCAGAACCTACTAGCAGCAGCAGTGAAGAAGTTGAGGAAAGTCTGCTGGGCT 121  
OY 143 GCAGACGCGATGATTAACGTCAGCCGAAATTAACATCGCCCTTCTGCTCAAGTGTG 202  
DB 122 GCAGACGCGATGATTAACGTCAGCCGAAATTAACATCGCCCTTCTGCTCAAGTGTG 181  
OY 203 AAGGCGCAGTGAAGATGCTGCGCGCTGATTAATCACTCACTGATCAACAGATTC 262  
DB 182 AAGGCGCAGTGAAGATGCTGCGCGCTGATTAATCACTCACTGATCAACAGATTC 241  
OY 263 ATGCTATGCTATCTGTTGGACATGATACAGAAACACAACTGACAGTGGTGA 322  
DB 242 ATGCTATGCTATCTGTTGGACATGATACAGAAACACAACTGACAGTGGTGA 301  
OY 323 GGGGCTTTGACACTTGTGACAGCAGTATGCTGTCGCGAGCGGGCCCTTATTTACGG 382  
DB 302 GGGGCTTTGACACTTGTGACAGCAGTATGCTGTCGCGAGCGGGCCCTTATTTACGG 361  
OY 383 AAGCTCTGTTCAATCCAGCGGCTCTTACCGAAACACCGTGCATGAATAAAGAG- 441  
DB 362 AAGCTCTGTTCAATCCAGCGGCTCTTACCGAAACACCGTGCATGAATAAAGAG- 421  
OY 442 AGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 501  
DB 422 AAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 481

OY	502	TCTTCAAAAAA	514
Dd	482	TCTTGCGAGAAA	494
RESULT 8			
Bf109912/c			
LOCUS			
DEFINITION	Bf109912	468 bp	mRNA linear EST 20-OCT-2000
	7171f03.X1 Soares.NSF_F8_9W_OT_PA_P.S1		Homo sapiens cDNA clone
	IMAGE:3526805	3	similar to TR:Q9U141 Q9U141 CHEMOKINE-LIKE FACTOR
ACCESSION	1.	[1]	; mRNA sequence.
VERSION	Bf109912		
KEYWORDS	Bf109912.1	GI:10939602	
SOURCE	EST.		
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1	(bases 1 to 468)	
AUTHORS	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: ccgaps-re@mail.nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Seq primer: -400P from Glibco.		
FEATURES	Location/Qualifiers		
source	1..468		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone IMAGE:3526805"		
	/clone_id="Soares.NSF_F8_9W_OT_PA_P.S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pTY73D-Pac (Pharmacia) with		
	a modified polylinker; Site:1: Not I; Site:2: Eco RI;		
	Equal amounts of plasmid DNA from five normalized		
	libraries were mixed, and ss circles were made in vitro.		
	Following HAP purification, this DNA was used as tracer in		
	a subtractive hybridization reaction. The driver was		
	PCR-amplified cDNAs from pools of 5,000 clones made from		
	the same 5 libraries. The pools consisted of the following		
	libraries and clones:		
	Soares NbHSF pool 1:		
	309384-310919, 333208-325885 Soares NbZHF pool 1:		
	145032-147335, 147720-148103, 148872-149255, 15002 -		
	150407, 151176-152327 Soares NbZHR8-9W pool 1:		
	758280-760583, 772104-774407 Soares NbHPA pool 1:		
	304776-306311, 320136-322893, 326280-326653 Soares NbHOT		
	pool 1: 723720-726407, 739080-740999 Subtraction by Benito		
	Soares and M. Fatima Bonalao."		
BASE COUNT	127 a	116 c	102 g
ORIGIN			123 t
Query Match	87.6%	Score 468;	DB 12;
Best Local Similarity	100.0%;	Pred. NO. 3.4e-60;	Length 468;
Matches 468;	Conservative 0;	Mismatches 0;	Indels 0;
		Gaps 0;	
OY	46	GGCGGTCCTCCGCCGCGGTGGCGGTTCTTAACGCTTCGCAGAACACTACTCAGCAGCCAG	105
Dd	468	GGCGGTGCTCCGCCGCGGTGGCGGTTGCTATACGCTTCGCAGAACACTACTCAGCAGCCAG	409
OY	106	CTGAAGAAGCTTGAGGAGAAAGTGTCTGCTGTGGGTCTGCAGACGCGCATGATGAACGTACA	165
Dd	408	CTGAAGAAGCTTGAGGAGAAAGTGTCTGCTGTGGGTCTGCAGACGCGCATGATGAACGTACA	349
OY	166	GCCCAATAATAAANTGGCCCCCTTCTGCTTAGTGTGAAGCCACGTAAGATGCTGCG	225
Dd	348	GCCCAATAATAAANTGGCCCCCTTCTGCTTAGTGTGAAGCCACGTAAGATGCTGCG	289
OY	226	GCTGATATTATTCACACTACTGTAACAACAGTATTCATAGTCAATGATGTTGTTGGC	285
Dd	288	GCTGATATTATTCACACTACTGTAACAACAGTATTCATAGTCAATGATGTTGTTGGC	229

OY	286	ACGATATCCGAGAAACCAACATTTGACAGTGTGGAGGGGTGTTGGACATTGGACAGC	345
Db	228	ACTATATCCAGAAACCAACATTTGACAGTGTGGAGGGGTGTTGGACATTGGACAGC	169
OY	346	AGATATGCTGTCCTCCGACGGGGCCCTTATTTTACCGGAAGCTTCGTTCATCCACAGC	405
Db	168	AGTATGCTGTCCTCCGACGGGGCCCTTATTTTACCGGAAGCTTCGTTCATCCACAGC	109
OY	406	TCCTTACCGAAAAAGCCTGTGCATGAAAAAAGAACTTTGTGATTTTATATTACTT	465
Db	108	TCCTTACCGAAAAAGCCTGTGCATGAAAAAAGAACTTTGTGATTTTATATTACTT	49
OY	466	TTAGTTGATCTAGTATTAACATATTTCTGATCTTCCAAAAA	513
Db	48	TTAGTTGATCTAGTATTAACATATTTCTGATCTTCCAAAAA	1
RESULT 9			
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LOCUS			linear
DEFINITION	BF01865968B1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098456 5', mRNA sequence.		EST 06-NOV-2000
ACCESSION	BF203359		
VERSION	BF203359.1		GI:11096945
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 930)		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-ref@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.n.gov Plate: L10CM965 row: h column: 17 High quality sequence stop: 537.		
FEATURES			
source	location/Qualifiers		
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	/clone_lib="NIH_MGC_17"		
	/tissue_type="rhabdomyosarcoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: muscle; Vector: pORF7; Site.1: EcoRI; Site.2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	318 a 203 c 257 g 152 t.		
ORIGIN			
Query Match	87.6%; Score 467.6; DB 12; Length 930;		
Best Local Similarity	98.6%; Pred. No. 2,4e-60;		
Matches 503; Conservative	0; Mismatches 4; Indels 3; Gaps 3;		
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Db	1	GCTGGGCGAGAGTAGGGGAGGGCGGTCTCCGCGGTGGCGGTTCATCGCTTCGC	60
OY	85	AGAACCTACCTAGCGACCGACCTAGAAAGATTTAGAGAAAGTCTGCTGTGGGTCTGC	144



Shanghai Institute of Endocrinology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64370045 (ex. 653332)  
Fax: 86-21-64743206  
Email: mbs@ems.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in  
Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers

```

BASE COUNT      149 a      112 c      145 g      120 t      7 others
ORIGIN
Query Match      81.0%; Score 432.4; DB 10; Length 533;
Best Local Similarity 95.5%; Pred. No. 5.6e-55;
Matches 487; Conservative 0; Mismatches 12; Indels 11; Gaps 4

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QY	13	AMGTGAAGCCGAGCTGTGGCGGAGAAAGTAAAGGAGGGCGGCTCTCCGCCGCGTGGCGGTTG	72
	35	AGGGGAGGCCGAGCTGGGCGGAGAAAGTAAAGGAGGGCGGTCTCCGCCGCGGTTGCGG---	6
QY	73	CTATGGCTTCGAGAACTACTCTACGAGCAGCCAGCTGAGAAAGATTGAGGAAAGTCTCTC	132
	92	CTATGCGCTTCGAGAACTACTCTACGAGCAGCCAGCTGAGAAAGATTGAGGAAAGTCTCTC	151
QY	133	TGCTGGGCTTCGAGAGCGGATGAGTAACGTCTCCAGCCGAAATTAACATCTGCCCTCTCG	192
	152	TGCTGGGCTTCGAGAGCGGATGAGTAACG--GCACCCGAAATTAACATCTGCCCTCTTNG	210
QY	193	CTTCAAGTGAAGGCCACGTGAAGATGCTCGGCTGGATTATTCACATCTGGTAAC	252
Db	211	CTTCAAGTGAAGGCCACGTGAAGATGCTCGGCTGGATTATTCACATCTGGTAAC	270
QY	253	AACAGATTCAATGCATCATGTATCTGTGTGTGGCACTGATACCAAGAAACCAACATTTGAC	312
Db	271	AACAGATTCAATGCATCATGTATCTGTGTGTGGCACTATACCAAGAAACCAACATTTGAC	330
QY	313	AGTTGGTGAGGGGCTTTGGCACTTGTGACAGCAGATGCTGTGTTGCCGAGGGGCCCT	372
Db	331	AGTTGGTGAGGGGCTTTGGCACTTGTGACAGCAGATGCTGTGTTGCCGAGGGGCCCT	387
QY	373	TATTTACGGGAAGCTTCTGTTCAATCCAGAGCGTCTTACCAAGAAAAGCTGTGCATTA	432

OY	433	AAAAAAAAAGAAATTTGTATTATTAATTACCTTATTGATTCAGCAAGAATAAACAATA	492
Dd	448	AAAAAACGAAG-----GTAATTATTAATTACTTTTAGTGATCAGTAAGATATAAACAATA	503
OY	493	TTTTCTGTATTCTTCCAAAIAAAAAAAAAAAAAA	522
Dd	504	TTTTCTGTATTCTTACAAAAAAAAAAAAAAAAAAAA	533

RESULT 13  
AA429945/c

LOCUS	AA429945	432 bp	mRNA	linear	EST 16-OCT-1997
DEFINITION	zw6f.f10.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:781291				
ACCESION	AA429945				
VERSION	AA429945.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 25, 2003, 11:55:49 ; Search time 1313 Seconds  
(without alignments)  
2194.347 Million cell updates/sec

Title: US-09-801-115b-2  
Perfect score: 508  
Sequence: 1 MDNVQPKIKHRPFCESVKGH.....LNPSPGYQKKPVHEKKEVL 99

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n model -DEV=xlp  
-Q/cgcn2.1/USPFO\_SPOOL/US09801115/runat\_20062003\_141102\_13583/app.query.fasta.1.263  
-DB=genembi -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human4.0.cdi -LIST=45  
-DOCAALIGN=200 -THR\_SCORE=DCT -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09801115.ecgn.1.1.3745 -runat\_20062003\_141102\_13583 -MCPU=6 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG  
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1: gb\_ba:\*  
2: gb\_hlg:\*  
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4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	515	6 AX061624	AX061624 Sequence
2	508	100.0	530	9 AF096895	AF096895 Homo sapi
3	471.5	92.8	655	9 AF057306	AF057306 Homo sapi
4	471.5	92.8	669	6 AX061665	AX061665 Sequence
5	471.5	92.8	688	9 BC004380	BC004380 Homo sapi
6	471.5	92.8	689	9 AF135380	AF135380 Homo sapi
7	366	72.0	485	11 G30204	G30204 human STS S
8	339.5	66.8	593	9 AF145216	AF145216 Homo sapi
9	331	65.2	434	9 AF135381	AF135381 Homo sapi
10	318.5	62.7	495	6 AX079435	AX079435 Sequence
11	275	54.1	523	10 AF253064	AF253064 Rattus no
12	245	48.2	207	6 AX330610	AX330610 Sequence
13	245	48.2	207	6 AX330787	AX330787 Sequence
14	245	48.2	207	6 AX331008	AX331008 Sequence
15	245	48.2	207	6 AX408097	AX408097 Sequence
16	238.5	46.9	682	10 AF253065	AF253065 Rattus no
17	227.5	44.8	568	10 AY047360	AY047360 Mus muscu
18	215	42.3	151620	2 AC018589	AC018589 Homo sapi
19	215	42.3	180702	9 AC018557	AC018557 Homo sapi
20	215	42.3	189460	9 AC010542	AC010542 Homo sapi
21	142	28.0	97083	9 AC010289	AC010289 Homo sapi
22	139.5	27.5	527	10 AY046597	AY046597 Mus muscu
23	115	22.6	69937	2 AC121275	AC121275 Mus muscu
24	115	22.6	150552	2 AC121952	AC121952 Mus muscu
25	108	21.3	6283	6 AX252052	AX252052 Sequence
26	108	21.3	6283	6 AX344430	AX344430 Sequence
27	108	21.3	6283	6 AX344835	AX344835 Sequence
28	102	20.1	6283	6 AX252053	AX252053 Sequence
29	102	20.1	6283	6 AX344431	AX344431 Sequence
30	102	20.1	6283	6 AX344836	AX344836 Sequence
31	88	17.3	45416	9 AC000090	AC000090 Homo sapi
32	86.5	17.0	700	9 AF278577	AF278577 Homo sapi
33	86	16.9	159074	2 AC128918	AC128918 Rattus no
34	85.5	16.8	13007	1 AE004148	AE004148 VLDLR ch
35	83.5	16.4	792	14 AF105732	AF105732 HIV-1 iso
36	83.5	16.4	792	14 AF105741	AF105741 HIV-1 iso
37	83	16.3	37948	6 AR166758	AR166758 Sequence
38	82.5	16.2	508	10 AF401530	AF401530 Mus muscu
39	82.5	16.2	1240	10 BC027684	BC027684 Mus muscu
40	81	15.9	627	14 AF094041	AF094041 HIV-1 iso
41	80.5	15.8	186873	2 AC115034	AC115034 Mus muscu
42	80.5	15.8	193819	2 AC116080	AC116080 Rattus no
43	79.5	15.6	64425	9 AL591368	AL591368 Human DNA
44	79.5	15.6	14457	2 AC023268	AC023268 Homo sapi
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## ALIGNMENTS

RESULT 1



AX061624  
LOCUS AX061624 515 bp DNA linear PAT 24-JAN-2001  
DEFINITION Sequence 29 from Patent WO0100806.  
ACCESSION AX061624  
VERSION AX061624.1 GI:12406709  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS dumas millne Edwards,J.B., Bougueleret,L. and Jobert,S.  
TITLE Complementary dna's encoding proteins with signal peptides  
JOURNAL Patent: WO 0100806-A 29 04-JAN-2001;  
GENSET (FRI)  
FEATURES  
source Location/Qualifiers  
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144..287  
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Pred. No.: 2 93e-56 Length: 515  
Score: 508.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-801-115B-2 (1-99) x AX061624 (1-515)  
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QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThValPheMetLeuIle 40  
DB 204 GTGAAGATGCTGGCTGGATATTAATCACTGTAACCAACAGTATTCATGCTCATC 263  
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
DB 264 GTATCTGTGTGGCACTGATACCAAGAACCAATGACAGTGGGGGGGTGTT 323  
QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeu 80  
DB 324 GCACCTGTGACACGAGTATGCTGCTCCGACGGGCCCTTATTTACCGAAGCTTCTG 383  
QY 81 PheAsnProSerGlyProTyrgLInLysLysProValHisGluLysGluValLeu 99  
DB 384 TTCAATCCAGCGGCTCTTACCAAGAAAGCCCTGTCATGAAAAAAGAGTTTTC 440  
RESULT 2  
AF096895 530 bp mRNA linear PRI 18-JUL-2001  
LOCUS AF096895  
DEFINITION Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.  
ACCESSION AF096895.2 GI:9989691  
VERSION AF096895.2  
KEYWORDS FLI\_CDNA.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS Han,W., Lou,Y., Tang,J., Zhang,Y., Chen,Y., Li,Y., Gu,W., Huang,J., Gul,L., Tang,Y., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R., Xia,D., Rui,M., Tang,J. and Ma,D.  
TITLE Molecular cloning and characterization of chemokine-like factor 1 (CKLF1), a novel human cytokine with unique structure and potential chemotactic activity  
JOURNAL Blochem. J. 357 (Pt 1), 127-135 (2001)  
MEDLINE 21308461  
PUBMED 11415443  
REFERENCE  
AUTHORS Han,W.L., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.  
TITLE Direct Submission  
JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38 Xue Yuan Rd., Beijing 100083, China  
3 (bases 1 to 530)  
REFERENCE  
AUTHORS Han,W.L.  
TITLE Direct Submission  
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China  
Sequence update by submitter  
On Sep 7, 2000 this sequence version replaced gi:6288733.  
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source Location/Qualifiers  
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148..447  
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/note="Increased expression in PHA stimulated cells;  
expression inhibited by IL-10"  
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Pred. No.: 3 04e-56 Length: 530  
Score: 508.00 Matches: 99  
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Query Match: 100.00% Indels: 0  
Gaps: 0  
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QY 1 MetaspasnaValGlnProLysIleLysHsArGProPhcYsPheSerValIysGlyHis 20  
DB 148 ATGATTAACGTGACACCGCAAAATAAACAATCCCTTCTGCTTCACTGTAAGGACAC 207  
QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThValPheMetLeuIle 40  
DB 208 GTGAAGATGCTGGCTGGATATTAATCACTGTAACCAACAGTATTCATGCTCATC 267  
QY 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
DB 268 GTATCTGTGTGGCACTGATACCAAGAACCAATGACAGTGGGGGGGTGTT 327  
QY 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeu 80  
DB 328 GCACCTGTGACACGAGTATGCTGCTCCGACGGGCCCTTATTTACCGAAGCTTCTG 387  
QY 81 PheAsnProSerGlyProTyrgLInLysLysProValHisGluLysGluValLeu 99  
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Db 388 TTCATCCAGCGGCTCCTTACAGAAAAGCCTGTGCATGAGAAAAAGAGTTTG 444

RESULT 3  
AF057306 655 bp mRNA linear PRI 31-DEC-1999  
LOCUS Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.  
DEFINITION AF057306  
ACCESSION AF057306 GI:6648618  
VERSION AF057306.1 GI:6648618  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE Zhang, J.S., Nelson, M., Wang, L. and Smith D.I.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic  
and Foundation, Rochester, MN 55905, USA

FEATURES  
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132..590  
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YIVTGEVAVILFFILLYLRDLRMLKWLFWPLDINSIVTFVFMILVSLALPE  
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BASE COUNT 171 a 137 c 153 g 194 t

ORIGIN

Alignment Scores:  
Pred. No.: 1,99e-51 Length: 655  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF057306 (1-655)

QY 1 MetaspasnavalglnprolysilleyshisarpopheserVallysGLYHis 20  
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Db 132 ATGGATTAACGTGCAGCGCGAAATAAACATCGCCCTTCTTCAAGTGTGAAGGCCAC 191  
21 Vallysmetleaurg----- 25  
192 GTGAAGATGCTGGCGCTGGCACTAGCTGACATCTATGACCTTTTATCATGCACAA 251  
25 ----- 25  
QY 252 GCCCTGAACATATATTGTTATCATCTGATTTGAAGTACACGTTATCTATTTCATA 311  
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Db 312 CTTTATATATGACTAGACTGATGATTAATGAAGTGGTATTGTCCTTTGCTTGAT 371  
28 IlelleasnsrleuValThrThValPheMetleuIleValSerValleuAlaLeuIle 47  
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Db 372 ATTATCAACTCACTGCTGAACAACAGTATTCATGCTATCTGTGTGGCACTGATA 431  
48 ProglutThrThleuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCys 67  
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Db 432 CCAGAAACCAACAATTCACATGTTGGAGGGGTGTTTGCACTTGTGACACAGTATGC 491

QY 68 CysleuAlaAspGlyValAlaLeuIleTyrArgGlySerleuPheAspProSerGlyProTyr 87  
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Db 492 TGTCTTCCGACGAGGGCCCTTATTTACCGGAAGCTTGTTCAATCCACAGCGCTTAC 551  
QY 88 GlnYslYsProValHisGlnYslYsGluValIleu 99  
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Db 552 CAGAAAAGCCTGTGCATGAGAAAAAGAGTTTG 587

RESULT 4  
AX061665 669 bp DNA linear PAT 24-JAN-2001  
LOCUS AX061665  
DEFINITION Sequence 70 from Patent WO0100806.  
ACCESSION AX061665  
VERSION AX061665.1 GI:12406789  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE dumas mline Edwards, J.B., Bougueleret, L. and Jobert, S.  
TITLE Complementary dna's encoding proteins with signal peptides  
JOURNAL Patent: WO 0100806-A 70 04-JAN-2001;  
GENSET (FR)

FEATURES  
source  
1..669  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
140..598  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC25025.1"  
/db\_xref="GI:12406790"  
translation="MDNVQPKIKHRPFCFSYKGVKMKRLALVTYSMTFFITQAPEP  
YIVTGEVAVILFFILLYLRDLRMLKWLFWPLDINSIVTFVFMILVSLALPE  
TTTTLVGGGVAVLTAVCCIALDGLIYRKLINPSGPYQKRVHEKREV."  
140..442  
sig\_peptide  
/note="Von Heljne matrix score 4.10 seq VEMILVSLALP/ET"

BASE COUNT 178 a 139 c 158 g 194 t

ORIGIN

Alignment Scores:  
Pred. No.: 2,04e-51 Length: 669  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 6 Gaps: 1

US-09-801-115B-2 (1-99) x AX061665 (1-669)

QY 1 MetaspasnavalglnprolysilleyshisarpopheserVallysGLYHis 20  
|||||  
Db 140 ATGGATTAACGTGCAGCGCGAAATAAACATCGCCCTTCTTCAAGTGTGAAGGCCAC 199  
21 Vallysmetleaurg----- 25  
200 GTGAAGATGCTGGCGCTGGCACTAGCTGACATCTATGACCTTTTATCATGCACAA 259  
25 ----- 25  
QY 252 GCCCTGAACATATATTGTTATCATCTGATTTGAAGTACACGTTATCTATTTCATA 319  
26 ----- 319  
Db 260 CTTTATATATGACTAGACTGATGATTAATGAAGTGGTATTGTCCTTTGCTTGAT 371  
28 IlelleasnsrleuValThrThValPheMetleuIleValSerValleuAlaLeuIle 47  
|||||  
Db 320 CTTTATATATGACTAGACTGATGATTAATGAAGTGGTATTGTCCTTTGCTTGAT 379  
48 ProglutThrThleuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCys 67  
|||||

Db	380	ATTATCACTACTGCTAAGCAACAGTATTCATGCATCAGTCATCGTGTGGCACTGATA	433
QY	48	ProglutThrThrThleuthThValglYglYValAlpheAlaLeuValThAlaValcys	67
Db	440	CCAGAAACCACACACTTGCACACTTGTGTGAGGGGGTGTGGCACTGTATCAGCACTATGC	499
QY	68	CysLeuAlaASPGLValAlaLeuIleYrArgLysLeuAlpheAsnProSecLysProYr	87
Db	500	TGTCTTGGCGAGGGGGCCCTTATTTACCGGAAAGCTTCTGTTCATTCACAGCGGCTTAC	559
QY	88	GlnLysLysProValHisGluLysLysGluValLeu	99
Db	560	CAGAAAAAGCCGTGTCATGAAAAAAAAGAGTTTGG	595
RESULT 5			
LOCUS	BC004380	688 bp	mRNA linear PRI 12-JUL-2001
DEFINITION	Homo sapiens, clone MGC:10658 IMAGE:3639550, mRNA, complete cds.		
ACCESSION	BC004380		
VERSION	BC004380.1	GI:13325133	
KEYWORDS	MGC.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 688)		
JOURNAL	Strausberg, R.		
	Direct Submission		
	Submitted (12-MAR-2001) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a>		
COMMENT	Contact: MGC help desk		
	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)		
	DNA Sequencing by: Genome Sequence Centre,		
	BC Cancer Agency, Vancouver, BC, Canada		
	<a href="mailto:info@bcsc.bc.ca">info@bcsc.bc.ca</a>		
	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,		
	Letitia Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,		
	Leticia Hsiao, Martin Krzywnicki, Reta Kutsche, Oliver Lee, Soo		
	Nes Lee, Victor Ling, Carrie Mathewson, Candice McLevy, Steven		
	Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline		
	Scheil, Duane Smalilus, Michael Smith, Lorraine Spence, Jeff Stott,		
	Michael Thorne, Miranada Tsai, Matasja van den Bosch, Jill Vardy,		
	George Yang, Scott Zuyderduyn, Marco Marra.		
FEATURES			
source	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a></p> <p>Series: IRAL Plate: 13 Row: F Column: 14</p> <p>This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9989692.</p> <p>Location/Qualifiers</p> <p>1..688</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="MGC:10658 IMAGE:3639550"</p> <p>/tissue="Pancreas, adenocarcinoma"</p> <p>/clone_id="NIH_MGC_39"</p> <p>/lab_host="DH10B-R"</p> <p>/note="Vector: pOTB7"</p> <p>137..595</p> <p>/codon_start=-1</p> <p>/product="Unknown (protein for MGC:10658)"</p> <p>/protein_id="AAH04380.1"</p> <p>/db_xref="GI:13325134"</p> <p>/translation="MDNVQPKIKHHPCESSGKHVMKRLATVTSMTPEIQAQAP YVITGGEVVLIFLITLVLRDRMKMLFMPFLDIINSVTTVMILYSVALIPE TTVITGGGAFALVTATVACCLADSLITRKLLENPSGYPQKPKVHEKEVY."</p> <p>201 a 138 c 154 g 195 t</p>		
CDS			
BASE COUNT			

[illegible]

gene /note="from PHA stimulated cells"  
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/gene="CKIF2"  
/note="UCK"  
148.606  
CDS /gene="CKIF2"  
/note="UCK-2; alternatively spliced"  
/codon\_start=1  
/product="chemokine-like factor 2"  
/protein\_id="AF19599.1"  
/db\_xref="GI:6630854"  
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YIVTGEVTVILFLLVLRDLKMLFWPLDIDINSIVTVMILVVALIPE  
TTTTLVGGVFAVLTAVCCADGALYIRKLIFNPSGPKYOKRVEKKEVL"  
BASE COUNT 195 a 140 c 161 g 193 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.11e-51 Length: 689  
Score: 471.50 Matches: 99  
Percent Similarity: 65.13% Conservative: 0  
Best Local Similarity: 65.13% Mismatches: 0  
Query Match: 92.81% Indels: 53  
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135380 (1-689)

QY 1 MetAspAsnValGlnProlysiLeuYshisArgProPhcysPheSerVallyslgYhis 20  
DB 148 ATGATACAGCTGACACCGCAAAATTAACATCGCCCTCGCTTCAGTGTGAAGGCCAC 207  
QY 21 VallyMelLeuArg----- 25  
DB 208 GTGAGATGCTGGCGTGGCAGCTACTGTGACATCATGACCTTTTATCATGCGACAA 267  
QY 25 ----- 25  
DB 268 GCCCGTGAACCATATATTGTATACACTGGATTGAATGACCGTATCTTATTTTCATA 327  
QY 26 -----Leuasp 27  
DB 328 CTTTATATGACTCAGACTTGATGCATTAATGACGTGTTATTTGGCTTGTGAT 387  
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47  
DB 388 ATATCACTGACTGATTAACAACATTCATCTCATGTCATCTGTGTGGCAGTATA 447  
QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67  
DB 448 CCGAAACACCAACATTTGACAGTGGTGGAGGGGTGTTGCACTTGTGACAGCAGTATGC 507  
QY 68 CysLeuAlaAspGlyAlaLeuIleTyraArglyslLeuLeuPheAsnProSerGlyProtyr 87  
DB 508 TGCTCTGGCGAGCGGGCCCTTATTACCGGAAGCTTCTTCATATCCAGCGGCTCTTAC 567  
QY 88 GlnLysLysProValHisGlnLysLysGluValLeu 99  
DB 568 CAGAAAAAGCCTGTGCATGAAAAAAGAGTTTTC 603

RESULT 7  
LOCUS G30204 485 bp DNA linear SMS 05-OCT-1996  
DEFINITION human SMS SHGC-36487, sequence tagged site.  
ACCESSION G30204  
VERSION G30204.1 GI:1593755  
KEYWORDS SMS; SMS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 485)  
AUTHORS Myers,R.M.  
JOURNAL Unpublished (1996)

## COMMENT

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu

Primer A: ACCTCTTTTTCATGACAGG  
Primer B: GCCCTTATTACCGAAGCT  
STS size: 77  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90565  
-- Washington University/Merk EST sequence.  
FEATURES  
source 1..485  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="16"  
STS  
primer\_bind 69..91  
primer\_bind complement(126..145)  
BASE COUNT 146 a 99 c 99 g 131 t 10 others  
ORIGIN

## Alignment Scores:

Pred. No.: 5.4e-38 Length: 485  
Score: 366.00 Matches: 73  
Percent Similarity: 98.65% Conservative: 0  
Best Local Similarity: 98.65% Mismatches: 1  
Query Match: 72.05% Indels: 0  
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x G30204 (1-485)

QY 26 LeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAla 45  
DB 286 CTTGATATTATCACTCAGTGTGAACACATTTATCATGCTCATCTGATGTTGGCA 227  
QY 46 LeuIleProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAla 65  
DB 226 CTGATACAGAAACCAACATTTGACAGTGTGGAGGGGTGTTGCACTTGTACAGCA 167  
QY 66 ValCysCysLeuAlaAspGlyAlaLeuIleTyraArglyslLeuLeuPheAsnProSerGly 85  
DB 166 GTATGCTGTCTGGCGAGCGGGCCCTTATTACCGGAAGCTTCTTCATATCCAGGGGT 107  
QY 86 ProTyraGlnLysLysProValHisGlnLysLysGluValLeu 99  
DB 106 CCTTACCGAAAAAGCCTGTGCATGAAAAAAGAGTTTTC 65

RESULT 8

AF145216	LOCUS	593 bp	mRNA	linear	PRI 07-SEP-2000
DEFINITION	Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,				
ACCESSION	AF145216				
VERSION	AF145216.2	GI:9989694			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Ma,D.L., Gu,W.F., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Han,W.L.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue				
REFERENCE	Yuan Road, Beijing 100083, China				
AUTHORS	2 (bases 1 to 593)				
TITLE	Direct Submission				
JOURNAL	Submitted (07-SEP-2000) Immunology, Peking University Health				
REFERENCE	Science Center, Xueyuan Road 38, Beijing 100083, China				
AUTHORS	Sequence update by submitter				
REMARK	On Sep 7, 2000 this sequence version replaced gi:6625671.				
COMMENT	Location/Qualifiers				
FEATURES	1..593				
source	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/cell_line="0937"				
	/note="from PHA stimulated cells"				
gene	1..593				
	/gene="CKLF4"				
	/note="CKLF4"				
	148..510				
CDS	/gene="CKLF4"				
	/note="CKLF4"				
	/note="VUC-4; alternatively spliced"				
	/codon_start=1				
	/product="chemokine-like factor 4"				
	/protein_id="AAF19350.1"				
	/db_xref="GI:6625672"				
	/translation="MDNWQPKIKRPFCSYKGVKMLRLALVTSMTFIIAQPAPR				
	YIVTGFGEVIVLFFILLYLRIIDRLMKMLFWPLIVLALVAVCCADGALYRKLLFF				
	NPSGPYKKRPVHEKEKYL"				
BASE COUNT	166 a 120 c 140 g 167 t				
ORIGIN					
Alignment Scores:					
Pred. NO.:	1.79e-34	Length:	593		
Score:	339..50	Matches:	73		
Percent Similarity:	61.90%	Conservative:	5		
Best Local Similarity:	57.94%	Mismatches:	15		
Query Match:	66.83%	Indels:	33		
DB:	9	Gaps:	2		
US-09-801-115B-2 (1-99) x AF145216 (1-593)					
OY	1	MetaspasnaValGlnpPolysIleIysHisArgProphCysPheSerValIysGlyHis	20		
Db	148	ATGGATTAACGGTCGACGCCGAATAATAAACATGCGCCCTTCCTCAGTGTAAGGCCAC	207		
OY	21	ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle	40		
Db	208	GTGAAGATGCTGGCGGTGGCAGCTA-----ACGTGACATTCATGACC	249		
OY	41	ValSerValIleuAlaIleuIleProGluThrThrThrIleuThrValGlyGly-----	58		
Db	250	TTTTTTATTCACGACCAAGCCCGTAACCATATATTGTTATCAGTGAATTTGAAGTCACC	309		
OY	58	-----	58		
Db	310	GTTATCTTATTTTTCATCACTTTTATATGACTCAGACTGTGATTCGATTATGATGAGTGTTA	369		
OY	59	-----ValPheAlaIleuValThrAlaValCysCysLeuAlaAspIleValA	73		

Df	370	TTTTGGCCTTGCTGTGTTTTCACATTGTGCACAGATAGCTGTCTTCCGACGGGCC	429
OY	74	LeuiletyrA-glySLeuIeuPhasnProSeRglyProtyrGlnIylsProvalHis	93
Df	430	CTTATTATACCAGAGCTCTGTGTCAATCCCGAGCTGCTTACGAAAAAGCCGTGCAT	489
OY	94	GluIylsLysGluValIeu 99 	
Df	490	GAATAAAAGAAGTTTTC 507	
RESULT 9			
LOCUS	AF135381	434 bp mRNA linear PRI 07-SEP-2000	
DEFINITION	Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,		
ACCESSION	AF135381		
VERSION	AF135381.2 GI:9989693		
KEYWORDS	.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D. Direct Submission Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China 2 (bases 1 to 434) Han,W.L. Direct Submission Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China Sequence update by submitter On Sep 7, 2000 this sequence version replaced gi.6630855. Location/Qualifiers 1..434 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_line="U937" /note="from PHA stimulated cells" 1..434 /gene="CKLF3" /note="vJCK" 148..351 /gene="CKLF3" /note="vJCK-3; alternatively spliced" /codon_start=1 /product="chemokine-like factor 3" /protein_id="AAPI9600.1" /db_xref="GI:6630856" /translation="MDNVQPKIKRPFCFSVKGHVKKMLRVFVALVTAVCCGLADALTY RKLLFNPSGPÖKRPVEKRKEVL"		
BASE COUNT	127 a	88 c	116 g 103 t
ORIGIN			
Alignment Scores:			
Pred. No.:	1.52e-33	Length:	434
Score:	331.00	Matches:	67
Percent Similarity:	67.68%	Conservative:	0
Best Local Similarity:	67.68%	Mismatches:	32
Query Match:	65.16%	Indels:	1
DB:	9	Gaps:	1
US-09-801-115B-2 (1-99)	x AF135381 (1-434)		
OY	1	MetaspasnaValGinProLyIleLysHisArgProPheCysPheSerValLysGlyHis	20
Df	148	ATGATTAACGTCGACGCGAAAATAAACATCGCCCTTCGCTCACGTGGAAGGCCAC	207
OY	21	VallysMetLeuArgLeuAspIlelleAsnSerIeuValInhrThrValPheMetIeuIle	40
Df	208	GTGAAGATGCTGCGCGCTG-----	225

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 Db 226 -----GTGTTT 231  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 Db 232 GCACCTGTGACAGCAGTATGCTGCTGCCGACGGGCGCTTATTACCGGAGCTCTG 291  
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGlyLysGluValLeu 99  
 Db 292 TTCATTCACGCGGCTTACCAGAAAGCCTGTGCTGCAAGAAAGAGAGTTTG 348  
 RESULT 10  
 AX079435 495 bp DNA linear PAT 22-FEB-2001  
 LOCUS Sequence 179 from Patent WO0107611.  
 DEFINITION AX079435  
 ACCESSION AX079435.1 GI:13158995  
 VERSION  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 495)  
 AUTHORS Baker, K.P., Goddard, A. and Wood, W.I.  
 TITLE Human polypeptides and methods for the use thereof  
 JOURNAL Patent: WO 0107611-A 179 01-FEB-2001;  
 Genentech, Inc. (US)  
 FEATURES  
 source location/Qualifiers  
 1..495  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 119 a 103 c 127 g 142 t 4 others  
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 Alignment Scores:  
 Pred. No.: 7.3e-32 Length: 495  
 Score: 318.50 Matches: 70  
 Percent Similarity: 56.45% Conservative: 0  
 Best Local Similarity: 56.45% Mismatches: 1  
 Query Match: 62.70% Indels: 53  
 DB: Gaps: 1  
 US-09-801-115B-2 (1-99) x AX079435 (1-495)  
 QY 1 MetAspAsnValGlnProLysIleLeuSHisArgProPheCysPheSerValLysGlyHis 20  
 Db 124 ATGGATTAACGTGCAGCGCAAAATTAACATCGCCCTTCTGCTCAGTGTGAAGCCAC 183  
 QY 21 ValLysMetLeuArg----- 25  
 Db 184 GTGAAGATCTGCGGCTGCGCACTAACTGACATCTATGACCTTTTATATATGACACAA 243  
 QY 25 ----- 25  
 Db 244 GCCCTGACCATATATTTGTATCACTGATTTGAAGTCACCGCTATCTATTTCATA 303  
 QY 26 -----LeuAsp 27  
 Db 304 CTTTATATAGTACTGAGACTGATGATTAAGAGGTGTTATTTGGCCTTGTGAT 363  
 QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47  
 Db 364 ATTATCACTCACTGATTAACACAGATTCATGCTATCTGTGTGGCAGTGA 423  
 QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67  
 Db 424 CCAGAAACCAACAACATTTGAGAGTGTGGAGGGGTGTTTGGACTGTTGACAGACAGTATGC 483  
 QY 68 CysLeuAlaAsp 71  
 Db 484 TGTNTTGGCGAC 495

RESULT 11  
 AF253064 523 bp mRNA linear ROD 27-NOV-2001  
 LOCUS Rattus norvegicus chemokine-like factor 1 (Ck1f1) mRNA, complete  
 DEFINITION  
 ACCESSION AF253064  
 VERSION AF253064.2 GI:17105378  
 KEYWORDS  
 SOURCE Rattus norvegicus.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 523)  
 AUTHORS Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-APR-2000) Immunology, Beijing Medical University,  
 Xueyuan Road, Beijing 100083, China  
 REFERENCE 2 (bases 1 to 523)  
 AUTHORS Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-NOV-2001) Immunology, Beijing Medical University,  
 Xueyuan Road, Beijing 100083, China  
 REMARK Sequence update by submitter  
 COMMENT On Nov 27, 2001 this sequence version replaced gi:7769680.  
 FEATURES  
 source location/Qualifiers  
 1..523  
 /organism="Rattus norvegicus"  
 /strain="Wistar"  
 /db\_xref="taxon:10116"  
 /tissue\_type="liver"  
 1..523  
 /gene="Ck1f1"  
 167..463  
 /note="Ck1f1"  
 /note="cytokine; similar to Homo sapiens Ck1f1"  
 /product="chemokine-like factor 1"  
 /protein\_id="AA069502.1"  
 /db\_xref="GI:7769681"  
 /translation="MDSPOKVDHQPCLSLKCFKVLRLDVIINSVVTTLEMLIVS  
 ALPEISTMIMVGVFGLTVICVADCALMCKLRPRRPGPPQNSAIDVDS"  
 BASE COUNT 134 a 107 c 133 g 149 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.14e-26 Length: 523  
 Score: 275.00 Matches: 53  
 Percent Similarity: 76.67% Conservative: 16  
 Best Local Similarity: 58.89% Mismatches: 21  
 Query Match: 54.13% Indels: 0  
 DB: Gaps: 0  
 US-09-801-115B-2 (1-99) x AF253064 (1-523)  
 QY 1 MetAspAsnValGlnProLysIleLeuSHisArgProPheCysPheSerValLysGlyHis 20  
 Db 167 ATGACATCTCCACAGAAAGTGTGAGACCATCAAGCCCTTGCCCATCTGAAATGCTTT 226  
 QY 21 ValLysMetLeuArgLysLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
 Db 227 GTGAAGACGCTGCGGTTGGATGATATCACTGCGGTGAACACATATTCATGCTTAT 286  
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60  
 Db 287 GTGCTGTGTGGCTGATATACCAAGAAACCAACATGATGATGTTGAGGGGTGTTT 346  
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80  
 Db 347 GGTTCCTGACAGATATATGATCTGCTGCTATGCTGCTTATGTCGCAAACTCCGG 406  
 QY 81 PheAsnProSerGlyProTyrGlnLysLys 90

```

Db      407 TTTCGTCCACATGACCTTATCAGAACAG 436
RESULT 12
AX330610/c      207 bp      DNA      1linear      PAT 09-JAN-2002
LOCUS      AX330610
DEFINITION      Sequence 1119 from Patent WO0194629.
ACCESSION      AX330610
VERSION      AX330610.1 GI:18103588
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1119 13-DEC-2001;
Avalon Pharmaceuticals (US)
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QY      92 ValHisGlnLysLysGlnValLeu 99
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AX330787/c      207 bp      DNA      1linear      PAT 09-JAN-2002
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DEFINITION      Sequence 1296 from Patent WO0194629.
ACCESSION      AX330787
VERSION      AX330787.1 GI:18103765
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1296 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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|||||
QY      72 GlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyrGlnLysLysPro 91
|||||
Db      145 GGGGCCCTTATTACCGGAGAGCTCTGTCATCCACGCGCTTACACGNAAGAGCCT 86
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QY      92 ValHisGlnLysLysGlnValLeu 99
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DEFINITION      Sequence 1517 from Patent WO0194629.
ACCESSION      AX331008
VERSION      AX331008.1 GI:18121642
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE      1
AUTHORS      Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1517 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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QY      72 GlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyrGlnLysLysPro 91
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Db      145 GGGGCCCTTATTACCGGAGAGCTCTGTCATCCACGCGCTTACACGNAAGAGCCT 86
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Db      85 GTGCATGAAAAAAGAGATTG 62
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AX408097/c

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 ACCESSION AX408097  
 VERSION AX408097.1 GI:21440802  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.  
 TITLE Gene expression profiles in liver cancer  
 JOURNAL Patent: WO 0229103-A 744 11-APR-2002;  
 GENE LOGIC INC (US)  
 FEATURES  
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 Db 145 GGGGCCCTTATTTACCGGAGAGCTTCTGTCAATCCACCGGCTCTTACCGAAGAAAGCCT 86  
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